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AF312211 AB018279 FR092H06 AE009810 AF144617

AJ288489 Homo sapi AF506010 Gallus ga

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SUMMARIES

Human DNA Human DNA

AL138734 AL583852

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ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. REFERENCE 1 (bases 1 to 190) AUTHORS HeideL., Arrondel, C., Forestier, L., Cohen-Solal, L., Mollet, G. TITLE 5tructure of the human type IV collagen gene COL4A3 and mutations in autosomal Alport syndrome JOURNAL J. Am. Soc. Nephrol. 12 (1), 97-106 (2001) MEDLINE 2004656 PUBMED 2 (bases 1 to 190) AUTHORS ALIGHAGA: AUTHORS ALIGHAGA: INTLE ALIGHAGA: AUTHORS ALIGHAGA:	Y Match Local Similarity 100.0%; Score 15; D Local Similarity 100.0%; Pred: No. 52 hes 15; Conservative 0; Mismatches 1 CCTTCTCCCCTGTT 15	ORGANISM Gallus gallus ORGANISM Gallus gallus ORGANISM Gallus gallus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. REFERENCE 1 (bases 1 to 600) AUTHORS Schneider, K., Kolthow, S., Schneider, P., Goebel, T., Kaspers, B. and Stachell, P. TITLE A chicken homolog of the B cell activating factor of the TNF family JOURNAL Unpublished REFERENCE 2 (bases 1 to 600) AUTHORS Schneider, K., Kolthow, S., Schneider, P., Goebel, T., Kaspers, B. and Stachell, P. TITLE Direct Submission JOURNAL Submission	Hermann-Herder-Str.11, Freiburg 79104, Germany Loation/Qualifiers 1600 /organism="Gallus gallus" /db_xref="taxon:9031" <1600 /gene="BAFF" <1534 /gene="BAFF" /codon_start=1
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Direct Submission

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Sequencing: Research Association for Biotechnology; cDNA library

construction, 5'- & 3'-end one pass sequencing and clone selection:

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University of Tokyo.
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2 (bases 1 to 1689)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligo capping; fis (full insert sequence).
Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to
mRNA, clone_lib:HEMBA1 clone:HEMBA1006278.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKO21867 1689 bp mRNA linear Homo sapiens cDNA FLJ11805 fis, clone HEMBA1006278, similar to POLY(A) POLYMERASE (EC 2.7.7.19).
                                                                                                                                                                                                                         5; Length 600;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HemBal1006278"
/tissue_type="whole embryo, mainly head"
/clone_lib="HEMBAl"
/dev_stage="embryo, 10 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="cloning vector: pME18SFL3"
186. .>1689
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                                                                                                                                                                                                                       Score 15; DB Pred. No. 47;
                                                                                                                                                                                                                                                                  0; Mismatches
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/db_xref="G1:10433147"
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AK021867/c
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Sus scrofa prophet of pit-1 (Prop-1) mRNA, complete cds.
AF232676.1 GI:11275672
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ARDTGLSEARIQVWFQNRRAKQRKQERSLLQPLAHLSPATFSGFLPEPPACPYSYPTP
PPPWTCFPHPYNHALPSQPSTGGSFARHPQSEDWYPTLHPTPTGHLPCPPAPPVLPLS
VMVEEFKQGLAVTDEILQGKSDWSKLLEPPNFFQKYRHYIVLTASASTEENHLEWVGL
VESKIRVLVGNLERNEFITLAHVNPQSFPGNKEHHKDNNYVSWMFLGIIFRRVENAES
VIDLITYDIQSFTDWYRNINMLKEGMKIEATHVKKKQLHHYLPAEIL"
309 c 366 g 459 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (Of-FEB-2000) Biology, Indiana University Purdue
University Indianapolis, 723 West Michigan Street, Indianapolis, IN
46202-5132, USA
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Sloop, K.W., McCutchan Schiller, A., Smith, T.P., Blanton, J.R. Jr.,
Rohrer, G.A., Meier, B.C. and Rhodes, S.J.
Biochemical and genetic characterization of the porcine Prophet of
Pit-1 pituitary transcription factor
Mol. Cell. Endocrinol. 168 (1-2), 77-87 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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McCutchan Schiller, A.L., Sloop, K.W., Blanton, J.R. Jr., Meier, B.C.
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2.1"
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                                                                                                                               Score 15;
Pred. No.
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/db_xref="taxon:9823"
1. .1721
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/gene="Prop-1"
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RESULT 7
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    CHKTGFBA/c
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DVTGTGEGAYMVYFVSFLGTLAVLPGNIVSALLMDKIGRLRKLAGSSWASCVSCFFLS
FGNSESAMIALLCLFGGVSIASWNALDVLTVELYPSDKRTTAFGFLNALCKLAAVIGI
SFTSFVGITKAAPILFASAALAGSSLALKLPETRGOVLO"
850 c 850 c 810 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be found
      PRI 12-JUL-2001
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 7 Row: 1 Column: 18 That Plate: 7 Row: 1 Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                  Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3190)
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                          gene product, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Similar to KIAA0736 gene product"
/protein_id="AAH00776.1"
/db_xref="GI:12653963"
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           linear
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/clone="IMAGE:359807"
/tissue_type="Brain, neuroblastoma"
/clone_lib="NIH_MGC_19"
/lab_host="PH108-R"
/note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
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3190 bp
Homo sapiens, Similar to KIAA0736
IMAGE:3509807, mRNA, partial cds.
BC000776
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                                                                                                                                                                                                                                                                                                                                                                                         Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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1. .3190
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Best Local Similarity 100.
Matches 15; Conservative
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AUTHORS
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RESULT 6

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FVFKPIFNISLLFLHCELTLCTNIDKDTQRLPKCVPPDEACTSLNVDMILAMMHNKKT
FYFRDIVITHEGKPEDSSLPKSNVRQPESVFYGLDTLTVVGIAPAAFVIGALITGALWFI
YSHTGEAGRRQVPFSSPASAHSIGSTQSTPGSSSSAT"
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VRT 21-JUL-1994
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1 (bases I to 334).

Barnett,J.V. Moustakas,A., Lin,W., Wang,X.F., Lin,H.Y., Galper,J.B. and Maas,R.L.

Cloning and developmental expression of the chick type II and type III TGF beta receptors

Dev. Dyn. 199 (1), 12-27 (1994)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (library: lambda zap) embryonic brain cDNA to mRNA.
Gallus gallus
CHKTGFBA 3347 bp mRNA linear VRT 21-JUL-
Gallus gallus transforming growth factor-beta type III receptor
                                                                                                                                                                                                                               plasma membrane; transforming growth
transforming growth factor-beta type III
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1. .3347
/organism="Gallus_gallus"
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/db_xref="GI:511843"
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152. 2677
/codon_start=1
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/dev_stage="embryonic"
/germline
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                                                                                                                                                                                     L01121.1 GI:511842
TGF-beta; betaglycan;
                                                                                                                                                                                                                                                                                  factor-beta receptor;
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Query Match
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ERLILEMYKIMAKROT YSINIGETGGGSTRAMIJARTCOLY PRAAASTLUHKKELVES
KWEWPNPULLKQPEESNILMPWDFRVNPSDRYHLMPIITPAYPQONSTYNVSTSRY
WWEERQGGAVTDEILIQGKSDWSKILLEPPRFCKYRHYINTASASTERNHLEWVGL
VESKIRVLUALERNEFIITAHVNPQSFGNREHHKDNNYVSUMFLGIIFRRVENAES
VNIDLTYDIOSFTDWYYRQANNINMIKEGMKIEATHKKNOLHYICPAEILIQKKKOG
LSDVNRSSGGLQSKRLSLDSSCLDSSRDTDNGTPFNSPASKSDSPSVGETERNSAEPA
                                                                                                                                                                                                                                    Direct Submission
Submitted (09-02T-2000) Surgery Branch, NCI, National Institutes of
Health, Building 10, Room 2847, Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVIVEKPLSVPPAQGLSIPVIGAKVDSTVKTVSPPTVCTIPTVVGRNVIPRITTPHNP
AQGQPHLNGMSNITKTVTPKRSHSPSIDGTPKRLKDVEKFIRLESTFKDPRTAEERKR
KSVDAIGGESMPIPTIDTSRKKRLPSKELPDSSSPVPANNIRVIKNSIRLILNR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKEMSANTVLDSQRQQKHYGITSPISLASPKEIDHIYTQKLIDA
MKPFGVFEDEEELNHRLVVLGKLNNLVKEWISDVSESKNLPPSVVATVGGKIFTFGSY
RLGVHTKGADIDALCVAPRHVERSDFFQSFFEKLKHQDGIRNLRAVEDAFVPVIKFEF
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                                                                               Identification and functional characterization of neo-poly(A) polymerase, an RNA processing enzyme overexpressed in human tumors Mol. Cell. Biol. 21 (16), 5614-5623 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to Homo sapiens poly(A) polymerase protein (PAP) encoded by GenBank Accession Number X76770" /codon_start=1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                    1 (bases 1 to 3752)
Topalian, S.L., Kaneko, S., Gonzales, M.I., Bond, G.L., Ward, Y. and
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Ohara,O., Suyama,M., Nagase,T., Ishikawa,K. and Kikuno,R.
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Topalian, S.L., Gonzales, M.I., Wang, X. and Wang, R.-F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="neo-poly(A) polymerase"
/protein_id="AAK83701.1"
/db_xref="G1:15080911"
                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="malignant melanoma"
232. .2442
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DNA Res. 5 (5), 277-286 (1998)
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RAESGGKGERMADGAPLAGVRGGLSDGEGPPGGRGEAQRRKEREELAQQYEAILRECG
HGRFQWTLYFVLGLALMADGVEVFVVGFVLPSAEKDMCLSDSNKGMLGLIVYLGMAYG
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Fugu rubripes cosmid 092H06 genomic DNA fragment, toplalpha gene.
AL035357
Direct Submission
Submitted (08-OCT-1998) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
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SVTHIKTIHQEDELIEIQSDTGTWYQRWGVRALSLGGQVWGNFLSCFGPEYRRITLAM
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GQYFNDKFIGLRLKSVSFEDSLFEECYFEDVTSSNTFFRNCTFINTVFYNTDLFEYKF
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TTAFGFLNALCKLAAVLGISIFTSFVGITKAAPILFASAALALGSSLALKLPETRGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (01-FEB-1999) Smith S.F., Fugu Group, UK HGMP Resource clocome Genome Campus, Hinxton Hall, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15; DB
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="KIAA0736 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith, S.F., Metcalfe, J. and Elgar, G. Unpublished
2 (bases 1 to 11001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1066
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                                                                                                                                        Location/Qualifiers
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100.0%;
                                                                                                                                                                                                                                                                                   /sex="male"
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Takifugu rubripes
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gene mRNA	CDS		exon	intron	intron	intron	intron	intron	intron

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VQQISTTDEVLNNPANIFVAQFFGDPPINILEGEGRGDHVDLGDLKIPIPARQGKLQV
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1 (bases 1 to 11896)
Fitz-Gibbon,S.T., Ladner,H., Kim,U.J., Stetter,K.O., Simon,M.I. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AE009810 11896 bp DNA linear BCT 16-JAN-2002
Pyrobaculum aerophilum strain IM2 section 65 of 201 of the complete
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GGREGDLLAAVRDELVYIDEVFDEIEGNDAEVLKEMLALLKRLEEKVEARLKKALGG"
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complement(601. .1404)
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/note="PAE1219"
/note="PAE1219"
/note="PAE1219"
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Fitz-Gibbon,S.T., Ladner,H., Kim,U.-J., Stetter,K.O., Simon,M.I.
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Submitted (12-DEC-2001) Microbiology and Molecular Genetics, University of California, Los Angeles, 405 Hilgard Ave, Los Angeles, CA 90095-1489, USA Angeles, CA 90095-1489, USA Location/Qualifiers

1. 11896

/organism="Pyrobaculum aerophilum" / Strain="IM2" / Ab_xref="Taxon:13773" / Ab_xref="Taxon:13
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/gene="toplalpha"
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/gene="toplalpha"
/number=20
/gene="toplalpha
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Avalos Ramirez, R., Orlich, M., Thiel, H.-J. and Becher, P. Complete genomic sequences of pestiviruses from giraffe and reindear: evidence for the presence of two novel species within the genus pestivirus
PPYYTPWAEVFNINPVFIGTEWERKIYCALHRLMSPGDILYVEYVDDRETFIALOKGE
APEATRLGALLRKCGFKIVKNWYHPEGGLEGGMKLQAVKV"
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The deases of to 12602)

Shecher, P. and Orlich, M.

Blicet Submission

Direct Submission

Submitted (21-ARR-1999) Justus-Liebig-Universitaet Giessen, Institut fuer Virologie (Fachbereich Veterinaermedizin), Frankfurter Str. 107, Giessen D-35392, Germany

E 5 (bases 1 to 12602)

S Avalos-Ramirez, R., Orlich, M. and Becher, P.

Direct Submission

L Submitted (26-MAR-2001) Justus-Liebig-Universitaet Giessen, Institut fuer Virologie (Fachbereich Veterinaermedizin), Frankfurter Str. 107, Giessen D-35392, Germany

Sequence update by submitter

On Aug 23, 2001 this sequence version replaced gi:6049239.
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetic diversity of pestiviruses: identification of novel and implications for classification Virology 262 (1), 64-71 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 12602)
Avalos Ramirez,R., Orlich,M., Thiel,H.J. and Becher,P.
Evidence for the presence of two novel pestivirus species
Virology 286 (2), 456-465 (2001)
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                                                                                                                                                            100.0%; Score 15; DB 1; Length 11896; 100.0%; Pred. No. 35;
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Pestivirus giraffe-1 H138 complete genome.
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Viruses; sSRNA positive-strand viruses,
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/product='conserved hypothetical protein"
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complement(7251. .7931)
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/gene="PAEL231"
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RVKKNIDDEPRVHTKLIVIDNQTVITGNINPTVSGFRRNKGVMLVIHNSTLARQLATIV
LNDFRGKYPRYNYPGVLVSPVNSQEGLEMIITLPGDLYIAMEQIYLDSGMVPLILQHO
RYYANVARUNADINIVAVDDDIVAKIIVVGDVYYVGSINLGYYSIQRNREVGLIHNPE
LAARLRALILQWYTEAGGVAPTETTETAAQPTTARTPAAQATAPSLIHALAMLVVVAI
  /translation="wwsEIFKDLDAFELGESALDVGAGFGNTTRYLLARGLRVCAVDI
DPGAVAYIKSLFKEFVKSGLLKVLLAPAESLPFADGECDSVISVAAVHHFRDIEVALR
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                                                                                                                                                                                                                                                           /transl_table=11
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                                                                                                                                                                                      /note="DNA metabolism; DNA replication, recombination, and
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/6469. 6850
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7987. .8274
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Matches

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1 CCTTCTCCCCCTGTT Similarity 15; Conser

Score 15; DB 14; Pred. No. 35;

Length 12602; Indels

SAIYLVLHYTMPQKYEVVGSCDRNQLNLTVKTRVEDVIPSSVWNIGKYVCVRPDWWPY ETTTVFIFEEVSQVVKLVLRALRDLTRIWNAASTTAFLICLVKVLRGQVIQGIVWLLL VTGAQGAITCEPEYQYALARSKRIGPLGAEDLVTTWHDYKFDLKIQDPLVMVYCKNDQ MKRCKAGYRFVSEBPCNREGVEISTRGKLKCIIEKTOVKVYAADNTLGPMPCKMEII SSEGPVSKTACTFNYTETLENKYFBRDEYEQQYMLKGKYQVWFDLKATDNRKDYFAE FLVIAVVALLGGRYVLWLLVTYFVITEQEASGLQLEPGVVVMIGNLITEDNIEVVYYF LTTLGMVVFLVLARRDPMLIPLVVAIATFKTTKYTAGFSVDVALAVLLIVLLICSYTS DYFKYRKLLQCLLSIGAAVFLIRSLKWLGGVGLPSIELPTQRPLFYILVYLIATALVT SWNLDIAGSLIQAVPILLLIFTLWADILTLILVLPTYELAKLYYLKMVKTDVEKTWTG GLPIFEASSGRVVGRVKVGKNEGAKPTKLMSGIQTVSKSTADITEMVKKIVAMNRGEF KQITLATGACKTTELPRSVVEEIGRHKRVLVLIPLRAAAESVYQYMRHKYPSIAFNLR IGEMKEGDMATGITYASYGYFCQMPQPKLRAAMVEYSYIFLDEYHCATAEQLAIIGKI AENALLVALEGYVGYQALSKRHIPIVTDIYTVEDHRLEDTTHLOFAPNAIRTDGKETE LKELAVGDIDRCTEAIADYTNKGIQFIKIQAANVMGSTAVKEVASEVKDYVQKFIDAL SESKEEILRYGLWGTHTALYKSIASRLGHETAFATLVIKWLAFGGESISDHIKQAATD PYAAQALKLFTPTRLESVYILSTAIYKTYLSIRKGKSDGLLGTGVSAAMEIMSQNPVS VGVAVMLGVGAVAAHNAIESCEQKRTLLMKVFVKNFLDQAATDELVKESPEKIIMALF EAVQTIGNPLRLIYHIYGVFYKGWETKDLAERTAGRNIFTLIMFEAVELLGVDSEGKI TVTTWLAYVFVDEDVGTIKPCLGEKVIPEKTGDVSLQSEVILDTTSVGISVVGGSDRA TTGITPVVIEKQSVTGGNQNILKIGLSEGEYPGPGVNRASISQAVEERDNRPWVLILG SDKATSNRVKTARNVRLYKGSDPVEVRRLMREGRLLVISLRDTDKGLHQYIDFKGTYL RKWHKFLDAITEHMTQVPVITADGEVYIREGQRGSGQPDTSAGNSMLNVLTMIYAFCE STGVPYRSFNRVAKIHVGDDGFLITEKSLGLKFASRGAQILHEAGKPQKILEGDRMK LLLFLVVRDEPVKKWVICLYHCLTMKPIKTAAVLVLLMSNVVNGEGGSKAGAGIDLYF NLVMKHKVRNDLVAKWYEDEEIYGMPKLVSIVKAASLSKTKSCILCTVCENKDWKGVN CPKCGGTGPPISCGMTLADFEERHYKRIFIREDSMNTMMCNRCQGKHRRFEMDREPKS ARYCAECNRLHPAEEGDFWAESSMLGLKITYFALMDGKVYDITEWAGCQRVGISPDTH RVPYHIPFGSRMPGTSDQREECEGFLQYRARGQLFLRNLPILATKVKFLMVGNLGSEV DSGCPDGARCYVLNPEAPNISGTKGAMVHLQKTGSEFTCVTASGTPAFFDLKNLRGWS HRFSDQLRVVAMTATPAGTVTTTGQKHPIEEFIAPEVMRGEELGSEFIDIAGLKIPTE EMKGNMLVFVPTRNMAVETAKKLKAKGYNSGYYYSGEDPANLKVVTSQSPYVVVATNA LEVLNNLLI SEDLPAAVKNIMARTDHPEPIQLAYNSYEVQVPVLFPKI RNGEVTDTYE TYTFLNARKLGEDVPAYI YATEDEDLAVDLLGLDWPDPGVQSTTETSRALKQVMGLST LVVYYIMNKPHFPGDTETQQEGRRFVASLLVAGLATYTYKTWNYNNLSKVVEPALACL IQGVVDFYYKGATIRVDTGNGKTVTATDKWEIDHATITRLLKKHTGIGFNGAYLGEEP NYKDLIGRDCATITRDSVQFLKMKRGCAFTYDLTLSNLVKLIELVHKNKLEERRIPEV PRETLEALSMGTPKAKQITKAEVRELLSPPSEDSGLPDWLTAENPVFLEATIRQEKYH IVGDVDVVKTKAKELGATDDTKIVKEVGARTYTMKLSSWFTQQSNKHHSLLPLFEEVL LQCPPKNPNPRVHMVSAYQLAQGNWEPVDCGVHLGTIPAKRSKTHPYEAYTKLKELLE EHKNSNEMGCGMVKEHNKWILRKIKHGNLRTKHILNPGKLSEQLARDGGKHNIYNKI IGSTMTSIGIKLEKLPVVRAQTDTTSFHDAIRDKIDKKENLQNPTLHTKLKEIFNNLS RPELRETYDEVDWGELEIGINRKGAAGFLEKKNIGEILTTEKKSVEEIIKKLRQGRLI VAFSFLLMYSWNPLVRRLCLMVMSKTHEVQPNKQAIYCYEGDPIAAYRDVIGHNLYEL KRTGFEKLASLNLSMSVLGIWTKHTSKRLIQDCIEVGKGDGNQLVNADRLVSSKTGHI YVPGSGYVVQGRHYEELSITKRPDRQTSNGLERYNLGPIVNLVLRRLRVMLMASIGRG LELPHQRGTRDIPTRLKDLPRKGDCRSGNNKGPVSGVYIKPGPVYYQDYSGPVYHRAP LELFEESTMCEVTRRLGRTTGSDGLLYHVYVCLDGCIIIKTASRAQQKVLKWTKNTLN CPLWLTSCSDEGGAKKKQVKPDRVEKGRMQIKPKESEKDSRTKPPDATIVLDGVKYQV KKKGKVKSKSTADGLYHNKNKPEOSRKKLEKALLAWAILAVLFOPVAGENITOWNLSD NGTSG1QHAMYLRGVNRSLHG1WPEK1CTG1PTHLATDTELKR1SGMMDASEETNYTC CRLORHEWNKHGWCNWFNIEPWIALMNRTQANLTEGPPPKECAVTCRYDKNTETNIVT **QARDRPTMLTGCKKGKNFSFAGTVIKGPCNFDVSLEDILFKDEGCGNMMQDAAIQEVD** GITNTVEGARQGAAKLTTWLGKQFRILGRKLEHKSKTWFGAHAASPYCEVNKKLGYIW YTNNCTPACLPGNTKIIGPGKFDTNAEDGKILHELGGHLSEFILLSLVVLSDFAPETA FFVGKRCKAGEARYLAKIHWRALPTSVVFEKVLEENPPEELPLEDNFEFGLCPCDSRP **VVKGNFNTTLINHSAFQLVCPIGWVGTIECTLVNTDTLATTVVKRYTRTTPFPMRAGC VVYKLIGEDLHHCTLGGNWTCVPEDDGTYTGGELEKCKWCGFKFRIPDGLPTYPIGRC** RVRYKRVTTVYDLEGSGEGVYLFPSKMGGRDGFDFTLPLLRAVLISCVSSYWQTFYLM YLAIDLLYYVHRKIIEEVAGGTNLASRLLAALIELNWTVDSEESKGLKKFFVLTSRVK GDLEHLGWVLRGPAVCKKITSHEKCHTGIADKLTAFFGIMPRGTTPRAPVRFPNALLK IRRGLETGWAYTHQGGISSVDHVTGGKDLLVCDSMGRTRVVCQSNNKMTDETEYGIKT IESGVTLPDLDVVVDTGLKCEKRVRISSKMPFIVTGLKRMAVTIGEQAQRRGRVGRVK PGKYYRSQETATGSKDYHYDLLQAQRYGIEDGINVTKSFREMNYDWSLYEEDSLLITQ RTLSSNYILDILHRLKNSLQISARKVIIGWAPAPFSCDWTASDDRIHLPSEDYQHIQT KCTCGYEMKAVKGADGKIVKVEEKGSFFCRNKYGRGPINHKVTRYYKGDMSEVKPMAK **NYYETAIPKNEKRDVNDDWEAGDLVTEKKPRVIQYPEAKVRLAITKVMYKWVKQKPVV** IPGYEGKTPLFLIFDKVKKEWDQFQDPVAVSFDTKAWDTQVTSRDLELIRDIQKYYFK VSHRFEDIEFCSHTPVPVRWADHTSSYMAGRNTATILSKMATRLDSSGDRGTAAYEKA

/product="structural glycoprotein E2" 2545 c 3288 g 2716 t

2447. .3568

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BASE COUNT

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KTIIOFDYRTDLESREEI NM CCERMITWLENALTHPEHTIDELTLLISDAREKELLARA
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GPDSPVAVLIERSERMITAIMGILKAGGAYVAIDPGFPAERIQYILEDCGADFYLTES
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ALTAYYRKNSIEATDGTPAHLQMLAAAGDFEGLKLKHMLIGGEGLSSVVADKLLKLFK
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LGREDDQVKVRGYR I ELGEI EAV I QQAPDVAKAVVLARPDEQGNLEVCAYVVQKPGSE
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SNSEGFRYSKAGARISGINPTPRVIETSFVLENSTPRQKIHVCVDFNIEMIERGGRSD
                                                                                                                                                              BCT 10-FEB-1999
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WSREETKKPLPLYDCDLFRFSLFTIKENEVWFYANVHHVISDGMSMNIVGNAIMHIYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAGTAPRLTNVYGPTETCVDASVHPVIPENAVQSAYVPIGKALGNNRLYILDQKGRLQ
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RNHSDTEGIIGMFVNTLAIRSEVKQNETFTQLISRVRKRVLDAFSHQDYPFEMLVEDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grandi, Eniricerche, Via F Maritano 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (28-JAN-1993) G. Grandi, Eniricerche, Via F Maritar
20097, S Donato Milanese (MI), ITALX
2 (bases I on 32802)
Cosmina, P., Rodriguez, F., de Ferra, F., Grandi, G., Perego, M.,
Venema, G. and van Sinderen, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence and analysis of the genetic locus responsible for surfactin synthesis in Bacillus subtilis
9336813
8355609
                                                                                                                  B.subtilis srfA-sfp gene region for surfactin synthetase. X70356 X70357 X70358 X70359 X70356.1 GI:396480 surfactin synthetase. Bacillus surfactin synthetase.
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/db_xref="taxon:1423"
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1. .10767
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Grandi, G.
DD 10231 CCTTCTCCCCCTGTT 10245
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> gene CDS

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**CRUENCHELBUNDTIENTLINGLEITLUGNIELE TEAMUGISTSKEULITGGETIDGETIDGETIGGETIGGETIGGETINGLEARKGER

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Z1580. . 25404

/ GORDE SETARA .

Z2580. . 255404 GASGQLY ITGQGLARGYLNRPQLTAERFVENPYSPGSLMYKTGDVVRRLSDGTLAFIG RADDQVKIRGYRIELGEIETVMLSLSGIQEAVVLAVSEGGLQELCAYYTSDQDIEKAE LRYQLSGLILPSHMIPAFFYQYDAIPLTANGKTPRNALRKPAAAQSGGKALAAPETALE ESLCRIWQKTLGIEGIDDNFFDLGGHSLKGMMLIANIQAELEKSVPLKALFEQPTV RQLAXYMEASAVSGGHQYLKPADKQDMYPLSSAQKRWYLNQLDRQTISYNMPSVLLM EGELDIWPARLTPQLVNRHESLRTSFMEANGEPVQRIIEKAEVDLHVFEAKEDEADQK HYIKEHGITYIKLTPSLFHTIVNTASFAFDANFESLRLIVLGGEKIIPTDVIAFRKMY GHTEFINHYGPTEATIGAIAGRVDLYEPDAFAKRPTIGRPIANAGALVLNEALKLVPP GDTIRFRIGSETAKAVEKLLÄETGTTLHMVLHAVFHVFLSKISGQRDIVIGSVTAGRT NADVQDMPGMFVNTLALRMEAKEQQTFAELLELAKQTNLSALEHQEYPFEDLVNQLDL • PRDMSRNPLFNVMVTTENPDKEELTLQNLSISPYEAHQGTSKFDLTLGGFTDENGIGL IKEFIRPFDLNDAPLIRAALLRIEAKKHLLLLDMHHIIADGVSRGIFVKELALLYKGE QLPEPTLHYKDFAVWQNEAEQKERMKEHEAYWMSVLSGELPELDLPLDYARPPVQSFK

gene CDS

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PLYDIOSQADQPKILDHIIVPENYPLODARMESSENGFDWYDVHYFEKSNYDLINLAA
SPGDEMLIKLAYNENVFDEAFILRLKSQLLTAIQOLIQNPDQPYSTINLVDDREREFE LTGLNPPAQAHETKPLTYWFKEAVNANPDAPALTYSGÖTLSYRELDEEANRIARRLOK HGAGKGSVVALYTKRSLEIVIGILGYLKAGAAYLPVDPKLPEDRISYNLADSAAACLL THQEMKEQAAELPYTGTTLFIDOGTRFEEQASDPATAIDPNDPAYINYTSGTTGKPKG TITTHANIOGLYKHVDYMAREDQDFFLSVSNYAFDAFTFDFVASMINAARLIIADEHT LLDTERLTDLILQENVNVMFATTALFNLLTDAGEDWMKGLRCILFGGERASVPHVRKA MEETIAQIWSEVLGRKQIGIHDDFFALGGHSLKAMTAVPHQQELGIDLPVKLLFEAPT IAGISAYLKNGGSDGLQDVTIMNQDQEQIIFAFPPVLGYGLMYQNLSSRLPSYKLCAF DFIEEEDRLDRYADLIQKLQPEGPLTLFGYSAGCSLAFEAAKKLEEQGRIVQRIIMVD LRIMGPGKLINCYGPTEGTVFATAHVVHDLPDSISSLPIGKPISNASVYILNEQSQLQ PFGAVGELCISGMGVSKGYVNRADLTKEKFIENPFKPGETLYRTGDLARWLPDGTIEY AGRIDDQVK I RGHRIELEEI EKQLQEY PGVKDAVVVADRHESGDAS I NAYLVNRTQLS **AEDVKAHLKKQLPAYMVPQTFTFLDELPLTTNGKVNKRLLPKPDQDQLAEËWIGPRNE**

Gaps ö 1; Length 32802; Indels ; DB 7 100.0%; Score 15; DE ilarity 100.0%; Pred. No. 32; Conservative 0; Mismatches | Similarity 15; Conserv Query Match Best Local S Matches 15,

1 CCTTCTCCCCCTGTT 15

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Louis

HTG.

KEYWORDS

SOURCE

ACCESSION VERSION

ORGANISM

AUTHORS TITLE JOURNAL MEDLINE PUBMED

REFERENCE

AUTHORS TITLE JOURNAL

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AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

AC107069/c LOCUS DEFINITION

RESULT 13

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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers inc. (http://www.resgen.com) or Pieter de Jong VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                         NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-495023, 2000 bp overlap;
The clone sequenced to the right is RP11-563C6, 2000 bp overlap.
Actual start of this clone is at base position 126621 of
RP11-495023.
McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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9623. 9918
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11997. 12065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                   AC107069 34578 bp DNA linear PRI 29-MAY-2002
Homo sapiens BAC clone RP11-249A8 from 2, complete sequence.
AC107069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (04-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 63108, USA
5 (bases 1 to 34578)
Waterston, R. H.
Direct Submission
Submitted (13-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 63108, USA
6 (bases 1 to 34578)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (29-MAY-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Apr 13, 2002 this sequence version replaced gi:19924179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (15-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 34578)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mapping information for this clone was provided by Dr. John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 34578)
Scott.K., Kozlowicz,A., Spalding,L. and Trani,L.
The sequence of Homo sapiens BAC clone RP11-249A8
Unpublished (2001)
3 (bases 1 to 34578)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                     Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: H_NH0249A08
                                                                                                                                                                                                                                                                                                                                                                                                        Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                          AC107069.5 GI:20146820
                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 34578)
29177 CCTTCTCCCCCTGTT 29163
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                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                            Homo sapiens
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Direct Submission

Direct Submission

Direct Submission

Submitted (21-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jun 8, 2000 this sequence version replaced gi:8247412.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations rotation may not be found in the sequence submission variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a note of the overlapping clone, as we submit sequences understain as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Bus. SMISSPROTY TT., TREMBL, We: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence chromosome 6, constructed by the Sanger Centre Chromosome 6 was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 was generated from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further WECTOR: pcrAPACP: The group of Pieter de Jong. For further IMPORTANT: This sequence is not the entire insert of clone RPI-310P17 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RPI-310P17 is at 1312P17 i
         Human DNA sequence from clone RP1-310P17 on chromosome 6. Contains
                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2281. .2431
/note=-7Alux repeat: matches 158. .308 of consensus"
2432. .2878
/note=="LiMM8 repeat: matches 5429. .5879 of consensus"
2879. .3641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1924. :2090

//note="Limm8 repeat: matches 6005. .6171 of consensus"

2151. :2266

/note="Limm8 repeat: matches 5874. .5991 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2879. .3641

//note="LTR17 repeat: matches 1. .780 of consensus"

3516. .4013

/note="match: GSS: Em:AQ112069"
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                           GSSs, complete sequence. AL138734
                                                                      AL138734.6 GI:8388469
                                                                                                                                                                                                     (bases 1 to 43347)
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                                                                                                               human.
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ORGANISM
      DEFINITION
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JOURNAL
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20561. .20610
/rpt_family="AT_rich"
21029. .21147
/rpt_family="MER1_type"
22335. .22201
                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="Malk"
18201. .18343
/rpt_family="CR1"
18517. .18822
/rpt_family="MER2_type"
19992. .20085
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20002. .20087
rpt_family="MER1_type"
20106. .20441
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/2467. .22528
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24482..24768
/rpt_family="L1"
25359..25381
/rpt_family="AT_rich"
26536..26845
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      /rpt_family="GA-rich"
12723. .12743
                                                               zus10. .28537
/rpt_family="AT_rich"
29081. .29460
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3468. .13770
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1061. .24481
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4609. .14696
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23765, .23897
/rpt_family="L1"
23988, .24016
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6430. .16990
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0451. .20530
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rpt_family="MaLR"
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.3881. .14194
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[4255. .14316
                                                                                                                                                                                                                                                                       .4609. .14696
'rpt_family="MIR"
.5519. .15572
                                                                                                                                                                                                                                                                                                                                rpt_family="Alu"
5951. .15997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'rpt_family="L2"
:2922. .23217
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Matches 15; Conservative 0
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15481. .15498

//note="AluS repeat: matches 152. .170 of consensus"

15499. .15731

/note="AluSyx repeat: matches 71. .308 of consensus"

15732. .15790

/note="AluS repeat: matches 1. .152 of consensus"

15822. .16105

/note="LiPal6 repeat: matches 5830. .6110 of consensus"

16106. .16416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Alusp repeat: matches 1. 313 of consensus"
16417. 1771
/note="LPAN6 repeat: matches 4517. 5830 of consensus"
17737. 18032
/note="MER61A repeat: matches 7. 314 of consensus"
18038. 18426
/note="LIPAN6 repeat: matches 4125. 4510 of consensus"
18038. 18426
/note="LIPAN6 repeat: matches 3826. 4124 of consensus"
18470. 18706
/note="LIMA repeat: matches 3826. 4124 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 59. .145 of consensus" 9753. .9893
/note="AluY repeat: matches 168. .311 of consensus" 10697. .1158
/note="L2 repeat: matches 2290. .2750 of consensus" 11255. .11286
/note="16 copies 2 mer ac 100% conserved" 11352. .11558
/note="HERWL repeat: matches 1757. .1969 of consensus" 112998. .13299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="wir repeat: matches 1, .208 of consensus"
14674. .14748
/note="LiME3 repeat: matches 5872. .5956 of consensus"
15052. .15480
/note="LiMe4 repeat: matches 3375. .3822 of consensus"
15481. .15498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18703. 19271.
/note="LiMD2 repeat: matches 5774. .6331 of consensus"
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                     .5429 of consensus'
                                                                                                                                                                                                                                                                                                                   589. .6721
note="AluSq/x repeat: matches 1. .133 of consensus"
                                                                                                                                                                                                                                                  /note="1.2 repeat: matches 2580. .2750 of consensus" 6304. .6577 totte="Alusx repeat: matches 9. .282 of consensus" 6589. .6721
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//note="L2 repeat: matches 1452. .2147 of consensus"

19893. .19948
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note="AluSp repeat: matches 1. .305 of consensus"
164. .7253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anote="AluJo repeat: matches 2. .289 of consensus" 8711. .8799
Anote="MIR repeat: matches 59. .145 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MIR repeat: matches 28. .143 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="MIR repeat: matches 47. .147 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1MB8 repeat: matches 5147.
                                           4063. .4518
/note="match: GSS: Em:AQ508138"
                                                                                                    /note="match: GSS: Em:AQ316392"
4657. .5169
                                                                                                                                                            'note="match: GSS: Em: AQ484379"
                                                                                                                                                                                                         /note="match: GSS: Em:AQ432756"
5449. .5596
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72594. .22733
72594. .22733
70014="match: GSS: Em:AQ357726"
70014="aatch: GSS: Em:AQ357726"
70014="12 repeat: matches 2620. .2710 of consensus"
70014="12 repeat: matches 2620. .2710 of consensus"
70014="12 repeat: matches 413. .509 of consensus"
70014="12 repeat: matches 413. .509 of consensus"
70014="12 repeat: matches 38. .312 of consensus"
70014="12 repeat: matches 2005. .2146 of consensus"
70014="12 repeat: matches 2005. .2146 of consensus"
70014="12 repeat: matches 61. .243 of consensus"
70014="12 repeat: matches 281. .1953 of consensus"
70014="12 repeat: matches 281. .3945 of consensus"
70014="12 repeat: matches 4. .346 of consensus"
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Human DNA sequence from clone RPI1-17G2 on chromosome 10, complete
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31290. .31366

/note="match: GSS: Em:AQ735362"

/note="match: GSS: Em:AQ735362"

/note="match: GSS: Em:AQ735362"

/note="match: GSS: Em:AQ735362"

/note="match: J1669

/note="J1R16c repeat: matches 102. .387 of consensus"

32151 .32455
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/note="Cheshire repeat: matches 723. .2420 of consensus"
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3318. .33468
..33468
/note="Charlie2 repeat: matches 327. .504 of consensus"
34076. .34305
/note="MIR repeat: matches 6. .260 of consensus"
34434. .34535
/note="L2 repeat: matches 2574. .2687 of consensus"
34633. .35136
/note="MER9 repeat: matches 1. .511 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28538. .29022 / Consensus / Co
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/note="Cheshire repeat: matches 27. .548 of consensus"
                                                                                                                                                                        of consensus"
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AL583852 AC011691
AL583852.6 GI:14702147
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Matches 15; Conservative
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GSS: Em: AQ083388"

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Submitted (03-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on or before Jul 12, 2001 this sequence version replaced
gi.7381811, gi:13396759.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
intis sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were ocvered by at least
one plasmid subclone or more than one M13 subclone; and the
absembly was confirmed by restriction digest. The following
the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT: Tr:, TREMBL; Wp:, MORNPEP; Information on the WORNPEP
then.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10
RP11-17G2 is from the library RPCI-11.1 constructed by the group of bleter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT: This sequence is not the entire insert of clone RP11-17G2 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-17G2 is at 56701 in this sequence. The true right end of clone RP11-397115 is at 2000 in this
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MER20 repeat: matches 103. .218 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MLT1I repeat: matches 68. .240 of consensus" complement(5738. .6110) /note="match: STS: Em:G53244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L2 repeat: matches 2645. .2749 of consensus"
477. .5644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2586. .2791
/notem"MIR repeat: matches 45. .258 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of consensus"
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/note="MER1B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="match: GSS: Em:AQ358591"
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note="match: GSS: Em:AQ812738"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        omplement(3478, .3937)
note="match: GSS: Em:AQ475942"
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/note="MIR repeat: matches 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .56701
/organism="Homo sapiens"
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/clone_lib="RPCI-11.1"
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/chromosome="10"
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                                                                   (bases 1 to 56701)
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                                                                                                          Chapman, J
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                                                                                                                                      TITLE
JOURNAL
                                                                       REFERENCE
                                                                                                          AUTHORS
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.568 of consensus"
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26933. .27097
                                                                                                              /note="L2 repeat: matches 2284. .2534 of consensus"
8947. .9112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.00ce="MER46C repeat: matches 7. .338 of consensus"
1870. .1878.
1870. .1878.
18833. .19044
/note="MIR repeat: matches 28. .260 of consensus"
7.00ce="MIR repeat: matches 5599. .5820 of consensus"
7.00ce="MIR repeat: matches 5599. .5820 of consensus"
7.00ce="MIR repeat: matches 5599. .5820 of consensus"
7.10ce="MIR repeat: matches 5599. .5820 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L2 repeat: matches 2242. .2521 of consensus"
16664. .16777
1010te="L2 repeat: matches 2596. .2708 of consensus"
16779. .16842
100te="16 copies 4 mer ggaa 81% conserved"
                                                                                                                                                                                                                                                                                                                                                  consensus,
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MER5A repeat: matches 18. .178 of consensus"
16288. .16546
                                                                                                                                                                                                                                                                                                    .2318 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    consensus,
                     /note="MER91A repeat: matches 5. .95 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2748 of consensus
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complement(2325, .25729)
/note="match: GSS: Em:AQ507252"
26471. .26619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MER5A repeat: matches 1. .188 of consensus" 27101. .27219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //note="13 copies 4 mer caca 82% conserved"
22199. .22596
//note="MSTA repeat: matches 1. .426 of consensus"
22480. .22743
//note="match: STS: Em:HS094YH3"
22597. .22638
22597. .22638
22599. .22638
                                                                                                                                                           /note="MIR repeat: matches 70. .248 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .214 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .200 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 13. .134 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .165 of consensus"
                                                                     .234 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // 16861. .16944
/note="21 copies 4 mer ggaa 75% conserved"
16951. .16994
/note="11 copies 4 mer ggaa 81% conserved"
17973. .18165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="10 copies 4 mer caca 92% conserved"
22770. .22846
//note="MIR repeat: matches 87. .165 of con
22959. .23149
                                                                                                                                                                                                                                                                       10458. .10642

/note="L2 repeat: matches 2129. .2318 of

13448. .13763

/note="MLT1A1 repeat: matches 1. .341 of

13847. .13898

/note="2".copies 26 mer 94% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1 repeat: matches 2136. .2213 of 24486. .24581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="48 copies 2 mer tt 63% conserved"
25073. .25451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16817. .16998
/note="7 copies 26 mer 62% conserved"
                                                                                                                                                                                                       /note="MLT1A1 repeat: matches 337.
9753. .10220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MER3 repeat: matches 1. . 23508 . . 23698 /note="L2 repeat: matches 2539 . 24378 . .24458
                                                                                                                                                                                                                                                       /note="match: GSS: Em:AQ497216"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 22.
18174. .18509
                                                                   /note="MIR repeat: matches 9.
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Anote="MIR repeat: matches 42. .164 of consensus"
31974. 32354
Anote="mill repeat: matches 1. .410 of consensus"
33596. 33015
Anote="mill repeat: matches 1. .410 of consensus"
Anote="mill repeat: matches 128. .547 of consensus"
33873. 34015
Anote="mill repeat: matches 50. .251 of consensus"
Anote="mill repeat: matches 50. .251 of consensus"
Anote="mill repeat: matches 50. .251 of consensus"
Anote="mill repeat: matches 46. .140 of consensus"
37028. .37195
Anote="Li repeat: matches 2137. .2276 of consensus"
Anote="Li repeat: matches 2137. .2276 of consensus"
37028. .37413
Anote="Li repeat: matches 2469. .2750 of consensus"
37014. .38057
Anote="Li repeat: matches 59. .220 of consensus"
Anote="Li repeat: matches 59. .220 of consensus"
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/note="MIR repeat: matches 31. .225 of consensus" 29356. .29488
/note="MIRSA repeat: matches 50. .184 of consensus" 29578. .29664
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7.note="MLTIC repeat: matches 5. .462 of consensus" 41719. .41924
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Query Match 100.0%; Score 15; DB 9; Length 56701; Best Local Similarity 100.0%; Pred. No. 31; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps

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Human kidney relat Extended human sec Escherichia coli p DNA encoding novel Plant resistance g Fusarium venenatum	ing no c tumo creati	Human digestive sy Bacillus lichenifo Canine EST-derived	Bacillus lichenifo Mouse Bcl-G polype	Arachidonic acid m Human breast cell Human foetal liver	#10649 brain	Frobe #9982 for ge	Probe #13933 used Probe #5747 used t	Human genome-deriv Porcine BAC-PIGF2-	Aspergillus oryzae	Pine O-methyl tran	Pinus radiata OMT Plant OMT enzyme D	Pine O-methyl tran Pinus radiata OMT	Human secreted pro	Plant dwarfing/stu	Arabidopsis thalia S. lavendulae MitH	Listeria monocytog Resveratrol syntha	Listeria monocytog	Tumour suppressor	Human secreted pro Rice 4-CL-specific	Human excretory re	Human novel polynu	Transcription cont Megakaryocyte kina	Human immune/haema	secreted	Human secreted pro Human secreted pro	Listeria monocytog Human prostate can	CABF-1 coding sequ	Sigma-54 factor 9 Propionibacterium	Human immune/haema	Drosophila melanog	coding n NF-ATp.	Lung cancer associ	lon	Drosophila melanog DNA encoding novel	prostate	Human prostate exp Strongylocentrotus
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The present sequence represents a probe for the A457P variant allele of a human norepinephrine transporter gene. The specification a method for succeptibility to sub-optimal norepinephrine transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine reansport in a target cell and treating susceptibility to impaired norepinephrine transporter cell and treating susceptibility to impaired norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, in humans in the subject or coaine or

amphetamine abuse.

Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene -

Robertson D, Blakely RD;

WPI; 2001-425681/45.

Claim 15; Page 69; 133pp; English

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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss. New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -Gaps ; 0 Length 15; Indels ; Score 15; DB 22; Pred. No. 38; Human secreted protein 5' EST, SEQ ID NO: 13316. Duclert A, Giordano J; Sequence 15 BP; 0 A; 8 C; 1 G; 6 T; 0 other; Mismatches . 0 AAC09241 standard; cDNA; 352 BP. 100.0%; 100.0%; 21-FEB-2000; 2000EP-0200610. 99US-0122487 (first_entry) Query Match 100. Best Local Similarity 100. Matches 15; Conservative 15 1 CCTTCTCCCCTGTT 15 Dumas Milne Edwards J, 1 CCTTCTCCCCCTGTT WPI; 2000-500381/45. (GEST) GENSET. Homo sapiens. EP1033401-A2. 06-OCT-2000 26-FEB-1999; 06-SEP-2000 AAC09241; RESULT 2 AAC09241/C g δλ

Claim 1; SEQ ID 13316; 71pp + CD-ROM; English.

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(e)
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
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25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                            cancer in a patient;
assessing the efficacy of a therapy for inhibiting prostate cancer
                                       selecting a composition for inhibiting prostate cancer in a patien assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient;
                                                                                                      (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                          Score 15; DB 23; Length 445; Pred. No. 32;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                  Sequence 445 BP; 109 A; 118 C; 109 G; 107 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #1856.
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                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                          100.08;
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                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS66052 standard; cDNA; 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                             370 CCTTCTCCCCTGTT 384
                                                                                                                                                                                                                                                                                                          1 CCTTCTCCCCCTGTT 15
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                                                                                                                                                                                                                                             Local Similarity
nes 15; Conserv
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                       in a patient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602 [all-length CDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                            Gaps
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, Otsuki T;
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                                                                                                               Length 549;
                                                                                                                                           Indels
                                                                                       Sequence 549 BP; 114 A; 178 C; 140 G; 117 T; 0 other;
                                                                                                                DB 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Nagai K,
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                                                              at ftp.wipo.int/pub/published_pct_sequences
                                                                                                               100.0%; Score 15; DB 100.0%; Pred. No. 32;
                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                  Human cDNA clone (5'-primer) SEQ ID NO:886.
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                                                                                                                                           Conservative
                                                                                                                                                                               423 CCTTCTCCCCTGTT 437
                                                                                                                                                                 1 CCTTCTCCCCCTGTT 15
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                                                                                                              Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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11-JAN-2000;
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detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH13642 are present human cDNA sequences; AAB92446 to AAH36993 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                     100.0%; Score 15; DB 22; Length 827; 100.0%; Pred. No. 31;
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Otsuki
                                                                                                                                                                                                                                                                       Sequence 827 BP; 264 A; 138 C; 199 G; 223 T; 3 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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ID AAH15437 standard; cDNA; 1689 BP.
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2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 CCTTCTCCCCCTGTT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCTTCTCCCCTGTT 15
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27-AUG-1999;
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particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAM103166 to AAM13628 and AAM13633 to AAM18742 represent human cDNA sequences; AAB92446 to AAM195893 represent human amino acid sequences; and AAM13629 to AAM13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a variant norepinephrine transporter. The specification a method for screening for susceptibility to sub-optimal norepinephrine (NE) transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the subject, the bubject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter genes are useful for gene therapy for modulating norepinephrine transport in a target
                                                                                                                                                                                                                                                                                                                                                                     Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine; amphetamine abuse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene -
                                                                                                                                                              Gaps
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                                                                                                                                    100.0%; Score 15; DB 22; Length 1689; 100.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                              DNA encoding human norepinephrine transporter variant A457P.
                                                                                                                                                              Indels
                                                                                                              Sequence 1689 BP; 555 A; 309 C; 366 G; 459 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "norepinephrine transporter"
                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                      AAH28083 standard; cDNA; 1854 BP
                                                                                                                                                          0;
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11-JAN-2000; 2000US-0175456.
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                                                                                     of the present invention.
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                                                                                                                                    Query Match
Best Local Similarity
Matches 15; Conserv
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                                   function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, hypertension, heart disease, psycho
cell and treating susceptibility to impaired norepinephrine transporter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           illness; hypertension; heart disease; stimulant abuse; cocaine;
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                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                       22; Length 1854;
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                                                                                                                                                                    Sequence 1854 BP; 356 A; 555 C; 493 G; 450 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding human norepinephrine transporter variant.
                                                                                                     stimulant abuse e.g. cocaine or amphetamine abuse.
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0
                                                                                                                                                                                                                                    100.0%; Score 15; DB
100.0%; Pred. No. 30;
ive 0; Mismatches
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1..1854
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2000US-0175456.
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Best Local Similarity 100.
Matches 15; Conservative
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2000US-0237039.
2000US-0237040.
2000US-0239935.
2000US-0249937.
2000US-0241221.
2000US-0241285.
                    2000US-0228924
2000US-0229343
2000US-0229343
2000US-0229345
2000US-0229345
2000US-02293513
2000US-0229513
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2000US-0231244
2000US-0231244
2000US-0231244
2000US-0231413
2000US-0232081
2000US-0232081
2000US-023239
2000US-023239
2000US-023239
2000US-0232400
2000US-0232401
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25-SEP-2000;
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29-SEP-2000;
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                                                                                                                                                                                                                                                                                                                          acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney fallure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                           Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
                                                   Gaps
                                                                                                                                                                                                                                                                                     hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
                                                  0;
                     100.0%; Score 15; DB 22; Length 1854; 100.0%; Pred. No. 30;
                                                  Indels
                                                                                                                                                                                                                                                   DNA encoding novel central nervous system protein #308
Sequence 1854 BP; 357 A; 554 C; 493 G; 450 I; 0 other;
                                                 Mismatches
                                                                                                                                                                     ABK43728 standard; cDNA; 2159 BP
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2000US-0205515.
2000US-0209467.
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2000US-0189874
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                                                                                          1362 CCTTCTCCCCCTGTT 1376
                                                   15; Conservative
                                                                            1 CCTTCTCCCCTGTT 15
                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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ABK43728
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The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to
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                                                                2000US-0249212.
2000US-0249213.
2000US-0249214.
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2000US-0249297.
2000US-0249299.
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2000US-0249264.
                2000US-0249209
2000US-0249210
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2000US-0249217.
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                  17-NOV-2000;
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The invention relates to isolated polynuclectide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The cand for chromosome cand gene malso used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving an expressing in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in capponastics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS6419-AAS94564 represent novel human DNA and
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from WIPO
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                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
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llarity 100.0%; Pred. No. 30;
Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                  DNA encoding novel human diagnostic protein #19092.
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                                                                                                                                           BP.
                                                                                                                      AAS83288/c
ID AAS83288 standard; cDNA; 2451
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23-AUG-2000; 2000US-0649167.
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                 1070 CCTTCTCCCCTGTT 1084
1 CCTTCTCCCCTGTT 15
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nes 15; Conserv
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                                                                                                     RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppressive; nootropic; neuroprotective; antiviral;
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                                                                                                                                                                                    ABL90474 standard; cDNA; 2520 BP
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164 CCTTCTCCCCTGTT 150
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P-PSDB; ABB90065.
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                                                                                                             RESULT 11
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Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
                                                                                                                                                                                                                                                                                                                 acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes, cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
                                                                                                                                                        DNA encoding novel central nervous system protein #584.
ABK44004 standard; cDNA; 2522 BP
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The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded to hovel central nervous system protein. (I) and polypeptides (III) encoded a pathological condition. Disorders which are disquosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, carebrovascular disorders e.g. cardiac farrest, carebrovascular disorders e.g. anglogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. corneal immunodeficiency virus (AIDS) and fungl, coular disorders e.g. dabotes e.g. corneal infection, gastrointestinal disorders e.g. dysphagia.

CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. lenkaemia, disorders involving neovascularisation e.g. malignancies, captre kidney failure and blood related disorders e.g. myocardial catter kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, for supporting cell culture of contained the contained the polypeptides can also be used to aid wound healing or contained the contained and in chemotrate; The
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ive 0; Mismatches
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                                                                                            2000US-0249300.
2000US-0250160.
2000US-0250391.
2000US-0251998.
2000US-0256719.
2000US-0256719.
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2000US-0251868.
2000US-0251869.
2000US-0251989.
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2000US-0254097.
2001US-0259678.
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Best Local Similarity 100.0%;
Matches 15; Conservative C
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P-PSDB; AAU87674.
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16-JUN-2000 (first entry)

Sequence 3580 BP; 734 A; 942 C; 1024 G; 880 T; 0 other;

ÖS

Human secreted protein clone as180_1 nucleotide sequence SEQ ID NO:159.

antibacterial; antifungal; cytostatic; antiinflammatory; dermatological; antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide; antithyroid; immune deficiency; severe combined immunedeficiency; SCID; infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus; connective tissue disease; multiple sclerosis; erythematosis; secreted protein; immunestimulant; immunesuppressant; virucide; rheumatoid arthritis; autoimmune pulmonary inflammation; asthma; Guillain Barre syndrome; autoimmune thyroiditis; myasthenia gravis; insulin dependent diabetes mellitus; graft-versus-host-disease; autoimmune inflammatory eye disease; allergy; ss. Human;

Homo sapiens.

WO200009552-A1.

24-FEB-2000

99WO-US18298 13-AUG-1999;

98US-0096815. 98us-0096622 14-AUG-1998 17-AUG-1998 04-SEP-1998 23-OCT-1998

98US-0105368. 99US-0115234. 99US-0119931. 99US-0120575 08-JAN-1999 12-FEB-1999 18-FEB-1999 30-APR-1999

(GEMY) GENETICS INST INC.

99US-0096622

4, LaVallie ER,
M, Agostino MJ,
Fechtel K; MCCOY JM, D, Treacy M Jacobs K, Merberg D Wong GG,

Collins-Racie LA, Evans C; Steininger RJ, Spaulding V;

WPI; 2000-205979/18. P-PSDB; AAY94977 New polynucleotides encoding secreted proteins, which may have e.g. nutritional, chemokine, immune stimulating or suppressing, hematopoiesis regulating, tissue growth, activin/inhibin antiinflammatory or tumor inhibition activity

Claim 168; Page 613-614; 641pp; English.

AAA16618 to AAA16697 encode the human secreted proteins given in AAA16618 to AAY94800, isolated from human adult brain, adult thyroid, adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult retina, adult testis, whole embryo, adult cartilage, kidney, and adult bladder. Constant adult bladder, constant proteins are polymore adult bladder, adult than a proteins are predicted to have blological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. The polymoreleotides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on Southern gels, and as chromosome or tags to identify chromosomes or to map gene positions. The proteins can be used in the treatment of immune deficiencies and disorders, such as severe combined immunedeficiency (SCID), as well as viral, bacterial, fungal and other infections. These infections include human immunodeficiency virus (HIV), hepatitis, herpesviruses, mycobacteria, Leismanda spp., malaria and condidiasis. The proteins can be used to treat autoimmune disorders such as connective tissue disease, multiple sclerosis, systemic lupus erythematosis, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host-disease and autolimume inflammatory eye disease. The proteins can also be used to treat allergic conditions, such asthma. AAA16698 to AAA16774 represent probes for the human secreted proteins from the present invention.

The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined

Claim 1; Page 85-86; 393pp; English.

immunodeficiency (SCID), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis), infectious disorders (e.g. heampatis), allergic conditions (e.g. asthma), neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis, coagulation disorders (e.g. heampobilia), and tumours. The polynucleotide sequences of the invention are also useful in gene therapy. ABK35610-ABK36232 represente cDNA sequences of the invention that encode for novel human secreted proteins.

DB 24; Length 3580;

Score 15;

100.0%;

Query Match

Sequence 3580 BP; 880 A; 1024 C; 942 G; 734 T; 0 other;

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                                                                                                                                                                                                                                          immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; altergic condition; neurodegenerative disorder; liver fibrosis; coaqulation disorder; gene therapy; antimicrobial; tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
                                                                                                                                                                                                                               Human secreted protein; hyperproliferative disorder; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Lavallie ER, Collins-Racie LA, Evans C;
Agostino MJ, Bowman MR, Spaulding V, Wong GG;
Howes SH, Resnick RJ, Gulukota K, Graham JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                          Gaps
                        0;
Length 3580;
                        Indels
                                                                                                                                                                                                         cDNA sequence #21 encoding novel human secreted protein.
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Score 15; DB 21;
Pred. No. 29;
                          Mismatches
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                                                                      2528 CCTTCTCCCCTGTT 2542
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Matches 15; Conservative
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Clark HF, Fechtel K,
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Merberg D,
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                               Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.

    (e) selecting a composition for inhibiting prostate cancer in a patient;
    (f) assessing the prostate cell carcinogenic potential of a compound;
    (g) determining whether prostate cancer has metastasized in a patient;
    (h) assessing the aggressiveness or indolence of prostate cancer in a

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                 Gaps
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(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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red. No. 29;
Mismatches
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2000US-189862P.
2000US-207454P.
2000US-211314P.
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166 CCTTCTCCCCTGTT 152

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Sequence 3
Sequence 5
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TUTLE OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 776; 37;
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US-09-484-970B-82
US-09-039-641-36
US-09-039-762A-36
US-09-013-612A-36
US-08-446-803-5
US-08-466-803-5
US-08-600-656-5
US-09-170-670-10
US-09-170-670-15
US-09-193-068-14
US-09-193-068-14
US-09-193-068-14
US-09-183-412-14
US-09-290-734-10
US-09-290-734-15
US-09-290-734-15
US-09-290-734-15
US-09-290-734-15
US-09-290-734-15
US-09-290-734-15
US-09-290-734-15
US-09-245-281-27
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US-09-245-281-27
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Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Walker, Michael G.
TILE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION UNDBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 86.7%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 37; Matches 13; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TTCTCCCCCTGTT 15
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NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 63552280 No. 6355228disk of No. 6355228th America, Inc.
STREET: 405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fuglsang, Claus Crone
TITLE OF INVENTION: An Oral Care Product Comprising A Mutan
Binding Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEM: DOS
SOFTWARE: CASTEM: US/09/295,744A
FILING DATE: O-Apr-1999
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                               OPERATING SYSTEM: PCF-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SORTWARE: DATONI DATA: US/08/619,542B
FILING DATE: June 21, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 4735.204-US
                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 42840-A-PCT-US
TELECOMMUICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.7%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 37; Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-295-744A-1

Sequence 1, Application US/09295744A

Patent No. 6355228

GENERAL INFORMATION:
                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                           FILING DATE: June 21, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTĒRISTICS:
LENGTH: 1419 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1020 CCTTCTCCCCCTG 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCTTCTCCCCTG 13
New York
:: New York
!RY: USA
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Gaps

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DB 4; Length 2431; 37;
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APPLICANT: Allen, Rebecca L.
APPLICANT: LORGAL, David M.
TITLE OF INVENTION: A Pollen-Specific Promoter From Maize
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOANGATEWS, Held and Malloy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2687;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.7%; Score 13; DB 1;
100.0%; Pred. No. 37;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                Score 13;
Pred. No.
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/911,532
FILING DATE: 09-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: POCHOPIEN, DATA
REFERENCE/DOCKET NUMBER: 32167
REFERENCE/DOCKET NUMBER: 92 P139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)707-8889
                                                                                                                     PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 500 W. Madison, 34th Floor
CITY: Chicago
STATE: 111inois
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08149695
Patent No. 5412085
                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                          86.7%; 3
100.0%;
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (312)707-9155
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 1...2431
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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; STRAIN: Line W22
US-08-149-695-8
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                                                            UNKNOWN
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                                                            ANTI-SENSE: UNI
ORIGINAL SOURCE:
ORGANISM: POI
MOLECULE TYPE: HYPOTHETICAL:
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US-09-221-017B-351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      86.7%; Score 13; DB 4; Length 1905; 100.0%; Pred. No. 37; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
COUNTRY: USA
ZIP: 94304-1018
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Feat-ESO for Windows
SOFTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
                                                                                                                                                                                                STRAIN: Trichoderma harzianum CBS 243.71
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 31-DEC-1997
PRIOR APPLICATION NUMBER: PP1546
FILING DATE: 30-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PCT/AU98/01023
APPLICATION NUMBER: PCT/AU98/01023
PRIOR APPLICATION NUMBER: PCT/AU98/01023
ATTONNEY, AGENT INFORMATION:
NAME: MONIOY, GLAddys H
REGISTRATION NUMBER: ACTAURAETH
NAME: MONIOY, GLAddys H
REGISTRATION NUMBER: ACTAURAETH
NUMBER: MONION, GLADYS H
REGISTRATION NUMBER: ACTAURAETH
NUMBER: MONION, GLADYS H
REGISTRATION NUMBER: ACTAURAETH
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NUMBER:
                                                                                                                                                                                                                              ) NAME/KEY: sig_peptide
) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-295-744A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 351, Application US/09221017B Patent No. 6444799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                           LENGTH: 1905 base pairs
                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 351:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2431 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 1568 CTTCTCCCCTGT 1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CTTCTCCCCCTGT 14
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              706141
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Gaps

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FILING DATE: 24-JAN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,695
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FILING DATE: 24-JAN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        663 TICICCCCTGIT 675
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TISSUE TYPE: Pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                        FILING DATE:
                                                      60661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-149-695-1
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                                                                                                                       Sequence 8. Application US/08377228
Sequence 8. Application US/08377228
Patent No. 5545546
GENERAL INFORMATION:
APPLICANT: ALLEN, Rebecca L.
APPLICANT: LONSOALE, David M.
TITLE OF INVENTION: A Pollen-Specific Promoter From Maize CORRESPONDENCE ADDRESS: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner STREET: 3000 K Street, N.W., Suite 500
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Allen, Rebecca L.
APPLICANT: Lonsdale, David M.
AITLE OF INVENTION: A Pollen-Specific Promoter From Maize
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                               COUNTY: USA

IIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/377,228
FLING DATE: 24 -JAN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/377,228
FLING APPLICATION DATA:
APPLICATION NUMBER: US/08/149,695
FILING DATE: 09-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/149,695
FILING DATE: 09-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
REGISTRATION NUMBER: 33229/290/PHHI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.7%; Score 13; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 37; ive 0; Mismatches
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ADDRESSEE: McAndrews, Held and Malloy
STREET: 500 W. Madison, 34th Floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08149695
Patent No. 5412085
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202,672-530)
TELEFAX: (202)672-539
TELEX: 904136
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2687 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
477 TTCTCCCCTGTT 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                       CITY: Was
STATE: D
COUNTRY:
                                                                                    RESULT 6
US-08-377-228-8
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Sequence 11, Application US/08377228

GENERAL INFORMATION:
APPLICANT: LONSDALE, David M.
TITLE OF INVENTION:
APPLICANT: LONSDALE, David M.
ADDRESSE: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: 18
CORREST: 3000 K Street, N.W., Suite 500
STATE: D.C.
COUNTRY: USA
CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Relaase HI.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.7%; Score 13; DB 100.0%; Pred. No. 37; tive 0; Mismatches
                                                                                                                                                                   CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US/07/911,532
FILING DATE: 09-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: POchopien, Donald J.
REGISTRATION NUMBER: 92 P139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)707-8889
TELEFAX: (312)707-8889
TELEFAX: (312)707-8889
TELEFAX: (312)707-9155
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2873 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,699
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Sequence 53, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENES
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                   ;
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. 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No. 36; ive 0; Mismatches
                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: MS-DOS
SOFTWARE: WOIDPERfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
PRIOR APPLICATION: 514
                                                                                                                                                                Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REGISCOPOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                   ;
                                                                                                                                                            86.7%;
100.0%;
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                                              Homo sapiens
                                                                                                                                                            Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (215) 568-554
TELEX: No. 5734039e
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                            298 TICICCCCTGII 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Pennsylvania COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 TICICCCCTGII 286
                                                                                                                                                                                                                                          3 TICICCCCTGIT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Penn Ce
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TTCTCCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                      ORIGINAL SOURCE:
ORGANISM: HOM
                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-08-306-691B-53/c
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US-08-770-301A-2/C
                                                                               ; NAME/KEY:
; LOCATION:
US-08-244-189-1
      ANTI-SENSE:
                                                               FEATURE
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APPLICANT: Kikuchi, Kimiko
APPLICANT: Kikuchi, Kimiko
APPLICANT: Miyoshi, Hivoyuki
APPLICANT: Miyoshi, Hivoyuki
APPLICANT: Kozu, Tomoko
TITLE OF INVENTION: No. 5580727el DNAs, Polypeptides Encoded Thereby
TITLE OF INVENTION: and Methods for Detecting the DNAs and Polypeptides
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                            86.7%; Score 13; DB 1; Length 2873; 100.0%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,189
FILING DATE: 15-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 37; Mismatches
                                                      FILING DATE: 09-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION UNMBER: 29,768
REFERENCE/DOCKET NUMBER: 33229/290/PIHI
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                        us 07/911,532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           760-183P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
18-08-244-189-1/c
Sequence 1, Application US/08244189
; Patent No. 5580727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INCOMMATION:
NAME: MITPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2873 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 7
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 205-8000
(703) 205-8050
FILING DATE: 09-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4287 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 205-805(
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 8110 Gatehov
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
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APPLICANT: Ohki, 1
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ADDRESSEE: No. 63352280 No. 6355228disk of No. 6355228th America, Inc. STREET: 405 Lexington Avenue CITY: New York STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09295744A
Patent No. 635528
GENERAL INFORMATION:
APPLICANT: Fuglsang, Claus Crone
TITLE OF INVENTION: An Oral Care Product Comprising A Mutan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13; DB 3; Length 4503;
Pred. No. 36;
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
APPLICATION NOMBER: US/09/175,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ_for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: ROZEK, CATOL
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 4735.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,744A
FILLING DATE: 20-APr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/770,301
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1422-287
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.7%; Scrillarity 100.0%; P. Conservative 0;
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INFORMATION FOR SEQ ID NO: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4503 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
: IDENTIFICATION METHOD:
US-09-175-581-2
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ZIP: 10174
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                      FILING DATE
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US-09-295-744A-12
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                                                    APPLICANT: IKEDA, JUN
APPLICANT: KANEDA, SUMIKO
APPLICANT: KANEDA, SUMIKO
APPLICANT: YANAGI, HIDEKI
APPLICANT: MATSUMOTO, MASAYASU
APPLICANT: YURA, TAKASHI
TITLE OF INVENTION: NOVEL STRESS PROTEINS
NUMBER OF SEQUENCES: 12
CORRESONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-175-581-2/c

Sequence 2, Application US/09175581

Patent No. 6034232

GENERAL INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: KANEDA, JUN
APPLICANT: WANGIT, HIDEKI
APPLICANT: YORA, TARASHI
TITLE OF INVENTION: NOVEL STRESS PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDER ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                      COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.7%; Scc. 100.08; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/770,301A FILING DATE: 20-DEC-1996 CLASSIFICATION: 435
Sequence 2, Application US/08770301A
Patent No. 5948637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MURRHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1422
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-205-8050
INFORMATION FOR SEQ ID NO., 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4503 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Conservative
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STRANDEDNESS: double
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                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22040-0747
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Matches 13; Conserv
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ZIP: 22040-0747
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Gaps

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Length 4411529; 0; Indels

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Query Match 86.7%; Score 13; DB 4; Best Local Similarity 100.0%; Pred. No. 27; Matches 13; Conservative 0; Mismatches (
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Job time : 1030.5 secs
                                                                                                                          US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09813133A
Patent No. 6452294
GREERAL INFORMATION:
APPLICANT: GAN, Weinlu et al
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001173
CURRENT APPLICATION NUMBER: US/09/813,133A
CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 55827
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APPLICANT: WHITE. Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
TILLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TILLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1 LA11529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37RV
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100.0%; Pred. No. 36;
tive 0; Mismatches
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LOCATION: 3188..5092

US-09-295-744A-12
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APPLICANT: FLEISCHMAN, Robert D.
                     LENGTH: 6032 base pairs
                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                       TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
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Matches 13; Conservative
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Matches 13; Conservative
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ORGANISM: Human
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US-09-813-133A-3/C
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US-09-103-840A-1
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Sequence 1203
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US-09-914-300-5909
US-09-914-300-5909
US-09-914-300-5909
US-09-914-300-5917
US-09-918-6-055-425
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113.573 Million cell updates/sec
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                                                                                              2002, 18:08:33 ; Search time 51.5 Seconds
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// Cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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Compugen Ltd.
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Result

Sequence 8838, Ap Sequence 18115, A Sequence 31719, A Sequence 17125, A Sequence 1826, Ap Sequence 21470, A Sequence 7574, Ap Sequence 3, Appli Sequence 3, Appli Sequence 2146, Ap Sequence 2146, Ap Sequence 2146, Ap	Sequence 2115, Apsequence 21, Appl Sequence 5718, Appl Sequence 5718, Appl Sequence 44, Appl Sequence 7270, Appl Sequence 2314, Appl Sequence 2807, Appl Sequence 2807, Appl Sequence 2807, Appl Sequence 405, Appl Sequence 405, Appl Sequence 2807, Appl Sequence 2807, Appl Sequence 2807, Appl Sequence 2807, Appl Sequence 405, Appl Sequence 2807, Appl Sequence 405, Appl Seque	Sequence 405, App Sequence 6353, Ap Sequence 61171, Ap Sequence 1171, Ap Sequence 7186, Ap Sequence 7188, Ap Sequence 7117, Ap Sequence 1517, Ap Sequence 1517, Ap Sequence 626, Ap Sequence 626, Ap Sequence 626, Ap Sequence 626, Ap Sequence 626, Ap	Sequence 1, Appliance 2008, Appliance 2188, Appliance 2189, Appliance 2189, Appliance 2189, Appliance 2189, Appliance 2189, Appliance 2189, Appliance 495, Appliance 2189, Appliance 3189, Appliance 216, Applia	Sequence 6005, Ap Sequence 4081, Ap Sequence 57, Appl Sequence 236, App
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US-09-783-590-3942 US-09-563-817-241 US-09-878-574-10802 US-09-878-574-14136 US-09-783-590-4961 US-09-783-590-4961 US-09-783-590-5058 US-09-923-876-4155 US-09-973-67-10118	US-09-783-990-96 US-09-783-590-184 US-09-864-761-31815 US-09-864-761-16964 US-09-924-400-23 US-09-924-400-23 US-09-864-761-21109 US-09-810-936-23 US-09-810-936-23 US-09-810-936-23 US-09-810-936-23 US-09-783-590-1369 US-09-783-590-1792	US-09-781-590-4487 US-09-960-352-12269 US-09-864-761-21082 US-09-987-701-9494 US-09-988-598-2298 US-09-974-300-6198 US-09-974-300-6198 US-09-974-300-6198 US-09-974-300-165 US-09-923-876-21 US-09-923-876-21 US-09-923-876-21 US-09-923-876-3401 US-09-783-590-573	US-09-923-876-307 US-09-964-824A-275 US-09-964-824A-275 US-09-974-300-3901 US-09-923-876-3393 US-09-923-876-33494 US-09-923-876-3404 US-09-923-876-3404 US-09-923-876-3201 US-09-923-876-3501 US-09-960-352-18318 US-09-960-352-18318 US-09-960-352-18318 US-09-923-877-43	US-09-986-774-110785 US-09-960-352-3963 US-09-864-761-27981 US-09-867-701-9096 US-09-867-701-9096 US-09-789-143-409 US-09-789-69-409 US-09-923-876-4628 US-09-923-876-4628 US-09-923-876-631 US-09-923-876-631 US-09-923-876-923
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Sequence 1577, Application US/09954456
Patent No. US20020115057A1
Patent No. US20020115057A1
APPLICAMT Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
        Sequence 195, App Sequence 3014, Ap Sequence 3011, Ap Sequence 2601, Ap Sequence 2601, Ap Sequence 4869, Ap Sequence 18515, A Sequence 1019, App Sequence 27, Appl Sequence 27, Appl Sequence 104, App Sequence 104, App Sequence 104, App Sequence 104, App Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 11, Appl Sequence 543, App Sequence 3114, App
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Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIN Ver. 2.0
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US-09-24-093B-3446
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US-09-864-761-18515
US-09-974-886-119
US-09-97-64-887-2606
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100.0%; Pred. No. 3.7;
ive 0; Mismatches 0;
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Matches 15; Conservative
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    RESULT 2
US-09-954-456-1577/c
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US-09-764-864-1704
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LENGTH: 15857
    TYPE: DNA
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1692
LENGTH: 8894
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
CHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7
US-09-864-761-13104
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT23
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PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13104
                           FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
                                                                            PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
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Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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OTHER INFORMATION:
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US-09-764-864-1692/C
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APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Profice TIC REFERENCE: DEX-027, CURRENT APPLICATION NUMBER: US/10/001,835
CURRENT FILING DATE: 2000-11-20
RIOMAREN OF SEQ ID NOS: 228
SOFTWARE: PatentIn version 3.1
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hone, Wensheng
TITLE OF INVENTION: BENEBERSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-20-4
PRIOR FILING DATE: 2000-20-4
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
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93.3%; Score 14; DB 10; Length 389;
100.0%; Pred. No. 15;
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2011-01-30
PRIOR FILING DATE: 2001-01-30
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Patent No. US20020048763A1
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Patent No. US20020160387A1
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Best Local Similarity 100.
Matches 14; Conservative
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; ORGANISM: Homo sapien
US-10-001-835-84
                           Best Local Similarity
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US-09-864-761-13104
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US-10-001-835-84/C
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  Query Match
                                                   Matches
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OTHER INFORMATION: MAP TO AC018506.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.7

OTHER INFORMATION: EXPRESSED IN PLACENRA, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.4

OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 4.4

OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN HERAT, SIGNAL = 9.1

OTHER INFORMATION: EXPRESSED IN HERAT, SIGNAL = 9.1

OTHER INFORMATION: EXPRESSED IN HERAT, SIGNAL = 9.1

OTHER INFORMATION: HERAT, SIGNAL = 9.1
                              PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 99/608,408
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFUMARE: Annomax Sequence Listing Engine VEFS: 1.1
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Pred. No.
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Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Weagher, Madeleine Joy
APPLICANT: Wang, Tongtong
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Best Local Similarity 100.0%;
Matches 13; Conservative 0
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ORGANISM: Homo sapiens
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US-09-922-217-616/c
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Patent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: ADOI-05-23
PRIOR PPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-4
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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                        Sequence 3063, Application US/09764877

Patent No. US20020147140a1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FIER REFERENCE: PC005

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3063

LENGTH: 8894
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Sequence 3349, Application US/09764877

Sequence 3349, Application US/09764877

Sequence 3349, Application:

TITLE OF INVENTION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PCOOS

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2.001-01-17

Prior application data removed - refer to PALM or file wrapper

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3349
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-877-3063
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US-09-764-877-3349
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Matches 14; Conserv
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US-09-764-877-3349/C
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US-09-764-877-3063
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Gaps

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DB 10; Length 209; 53;

Gaps

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APPLICANT: Elsenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION UNDBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: CAMPOSITIONS SOF OVARIAN CANCER FILE REPERENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FASISEQ for Windows Version 4.0
ENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 315;
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100.0%; Pred. No. 52;
iive 0; Mismatches
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PRIOR PILLING DATE: 2000-01-28
PRIOR FILLING DATE: 2000-01-28
PRIOR FILLING DATE: 2000-01-28
PRIOR FILLING DATE: 2000-02-01
PRIOR FILLING DATE: 2000-02-01
PRIOR FILLING DATE: 1999-01-29
PRIOR FILLING DATE: 1999-01-29
PRIOR FILLING DATE: 1999-02-01
PRIOR FILLING DATE: 1999-03-26
PRIOR FILLING DATE: 1999-03-26
PRIOR FILLING DATE: 1999-05-14
PRIOR FILLING DATE: 1999-11-12
PRIOR FILLING DATE: 1999-11-12
PRIOR FILLING DATE: 1999-11-12
PRIOR FILLING DATE: 1999-11-12
SOFTWARE: FASTERE OF WINDER: 60/165,086
PRIOR FILLING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
LENGTHAN: 315
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; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 96, Application US/09712363
Patent No. US20020164588A1
GENERAL INFORMATION:
         Harlocker, Susan L.
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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US-09-867-701-4769
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US-09-867-701-10110/c
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Fatent No. US20020110547A1
GENERAL INFORMATION
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: PastSEQ for Windows Version 3.0
SOFTWARE: AND Off
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                                                                  APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FatLSEQ for Windows Version 4.0
SEQ ID NO 616
LENGTH: 210
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Patent No. US2002013237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; LCCATION: 156, 181, 194
; OTHER INFORMATION: n = A,T,C or G
US-09-922-217-616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc_feature
; LCCATION: (1)...(210)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-263-616
Jiang, Yuqiu
Smith, Carole Lynn
King, Gordon E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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Search completed: December 11, 2002, 20:32:36
Job time: 75.5 secs
                                       13; Conservative
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                                       Matches
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1 Patent No. US20020115057A1
2 Sequence 892, Application US/09954456
2 Patent No. US20020115057A1
3 Sequence 892, Application US/09954456
3 Sequence 892, Application US/09954456
3 PAPLICANTY Young, Paul
3 TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents US/09954
3 FILE REFERENCE: 809290-76
3 CURRENT APPLICATION NUMBER: US/00/233,617
3 PRIOR PLICATION NUMBER: US/00/234,052
3 PRIOR PLICATION NUMBER: US/00/234,923
4 PRIOR PLICATION NUMBER: US/00/235,134
4 PRIOR PLICATION NUMBER: US/00/235,134
5 PRIOR PLICATION NUMBER: US/00/235,134
5 PRIOR PLICATION NUMBER: US/00/235,134
5 PRIOR PLICATION NUMBER: US/00/235,131
5 PRIOR PLICATION NUMBER: US/00/235,720
5 PRIOR FLING DATE: 2000-09-27
6 PRIOR FLING DATE: 2000-09
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Sequence 10110, Application US/09867701
Fatent No. US20020132337a1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Adlate, Paul A.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER; TITLE OF INVENTION: UND DIAGNOSIS OF OVARIAN CANCER; CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastEED for Windows Version 4.0
LENGTH: 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

86.7%; Score 13; DB 10; Length 337;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 0; Indels
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ORGANISM: Homo sapien
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Scoring table: Perfect score: Sequence:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CHINATION	dP		Score Match Length DB ID De	15 100.0 181 17 AZ284882 AZ284882 AZ284882 RPCT-23	15 100.0 226 10 AV335397 AV335397 AV335397 AV33539	246 9 AL708655	297	378 14 F07213	393 14 T08889
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Contact: Shaying Zhao
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BG231740
                                                                                                                                                                                                                                 AW296329
BB836778
BF291788
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BE810065
                                      BF365993
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                                                                                                                                                                                 BH873765
                                                                                                                                                                                                                                                          BH785148
AI424915
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Mus musculus
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
Tel: 301 838 0200

Email: szhao¢tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieterd@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

Plate: 442 row: E column: 20
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                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="rpc1-23-442E20"
/clone_lib="RPCI-23"
/sex="Female"
                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                        Location/Qualifiers
1..181
                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
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297 bp mRNA linear EST 24-JUN-1999 AV067076 Mus musculus small intestine C57BL/6J adult Mus musculus AV067076
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Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, Kikuchi, N., Kojima, Y., Matsuyama, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Itoh, M., Izawa, M., Swato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tareno, M., Tomaru, Y., Tominaga, N., Mutanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Okazaki, Y. and Hayashizaki, Y.
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Fax: 81-298-36-9098
Fax: 81-298-36-9098
Fmail: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
      Heubner, D., Mewes, H.W., Weil, B. and Wiemann, S.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                           Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s. Wiemann@dkfz- heidelberg.de;
Sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp686J0853) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@tzpd.de.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DkFzp666J0853"
/clone=lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15; DB 9; Pred. No. 5.5e+02; 0; Mismatches 0;
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Genome Science Laboratory
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                                                                 Contact: Wambutt R
MIPS
   EST (Wambutt, R., He
Unpublished (1999)
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                                                                                                                                                   Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. 463-470 (1999).

Carninci, P. and Hayashizaki, Y. 463-470 (1999).

Carninci, P. and Hayashizaki, Y.

High efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RIKEN full-length enriched, adult male medulla oblongata"
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DKF22686J0853_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
AL708655
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Email: genome-res@gsc.riken.go.jp,
WEL:http://genome-gsc.riken.go.jp,
Saski,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 246)
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Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
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/dev_stage="adult"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="6330571M18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 c
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Gaps

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/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old:
isolate=muscular atrophy patient; tissue_type=total brain;
total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
a 111 c 99 g 9 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUBB89 393 bp mRNA linear EST 03-AUG-1993 EST06781 Infant Brain, Bento Soares Homo sapiens CDNA clone HIBBL71 5' end similar to p87 transporter-like protein, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 39)

Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C. Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library Nat. Genet. 4, 373-380 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="ATCC (inhost):85383"
/db_xref="taxon:9606"
/clone="HIBBLI"
/clone="HIBBLI"
/clone="Vector: Lafmid: The IB library was constructed by directional cloning and oligo(dT)-priming in the Lafmid vector, utilizing a three month old infant human brain (total brain)."
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The Institute for Genomic Research
302 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: mdadams@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                 Score 15; DB 14;
Pred. No. 5.6e+02;
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                                                                                                                                                                                                                                                                                        /tissue_type="small intestine"
/dev_stage="adult"
/dev_stage="adult"
/note="Organ: mammary gland; Vector: pr773D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st_strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSCIZB021 normalized infant brain cDNA Homo sapiens cDNA clone C1zb02, mRNA sequence. F07213 G1:672862
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0
                                                                           /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2010200P09"
/clone_lib="Mus musculus small intestine C57BL/6J adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 378)

Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Sebastiani Rabaktchis, C. and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome of the expression

C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
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Seq primer: (-21)Ml3_universal.
    Location/Qualifiers
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1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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//db_xref="taxon:9606"
//clone="c-1zb02"
//clone_lib="normalized infant brain cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 15; DB 9; I
100.0%; Pred. No. 5.5e+02;
ive 0; Mismatches 0;
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/tissue_type="total brain"
                                                        /organism="Mus musculus"
details.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genexpress@genethon.fr
Single read.
                                                                                                                                                                                                                                                                                                                                                                                                                                  79 g
                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Genethon
Genexpress-Genethon
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Matches 15; Conservative
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Fax: 33160778698
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further
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Hali,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajandream,M.A. and Barrell,B.G.

Lonetted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Submitted (10-DEC-2000) Trypanosoma brucei genome Campus, Hinxton,

cambridge CBIO 18A, E-mail: barrell@sanger.ac.uk and

nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TRED927/4 GUTAt 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Barrell, Oxford University Press, 1999).

Banil: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers

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DNA clone 8e07, forward sequence, genomic
                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 399)
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                                                                                                                                                                                                                                                                                                    Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Gallus gallus bursal lymphocyte EST
Unpublished (2002)
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="22g1lr1"
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Heinrich-Pette-Institute
                    AJ449549.1 GI:20216770
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                                                                                                                                                                                                                                              Contact: Buerstedde JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trypanosoma brucei.
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AL452614
                                                                                 Gallus gallus
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Matches 15; Conserv
AJ449549
                                                            chicken.
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AUTHORS
TITLE
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TA8E07P
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Mashu Zebrafish EST Project 1998
Washu Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Smail: zbrafish@watson.wustl.edu
Library constructed by: Chandra Tucker and Gregory Niemi DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution: RessourcenZentrumPrimarDatenbank, Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B1706542 403 bp mRNA linear EST 13-FEB-2002 fq07c03.yl Zebrafish adult retina cDNA Danio rerio cDNA clone 4790765 5' similar to TR:Q9UH03 Q9UH03 BK250D10.3 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 403)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S.L., Hiller, L., Rucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
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/note="Vector: Lambda ZAP II (pBluescript SK-); Site_Econst; Site_2: Sall; This Zebrafish library was constructed by Dr. Susan E. Brockerhoff (email: sbrocker@u.washington.edu) RZPD library number: 760"
a 89 c 116 g 93 t
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100.0%; Pred. No. 5.6e+02;
tive 0; Mismatches 0;
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100.0%; Pred. No. 5.6e+02;
iive 0; Mismatches 0;
/organism="Trypanosoma brucei"
/strain="TRD0927"
/db_xref="taxon:5691"
/clone="8e07"
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Location/Qualifiers
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Seq primer: T3 ET from Amersham
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/db_xref="taxon:7955"
/clone="4790765"
                                                                                                                     118 g
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BI706542.1 GI:15682237
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Best Local Similarity 100.
Matches 15; Conservative
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Gaps

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human.

SOURCE ORGANISM

AUTHORS TITLE

JOURNAL

REFERENCE

DEFINITION RESULT 10 AW139708/c

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ACCESSION VERSION KEYWORDS

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420 bp mRNA linear EST 02-MAR-2000 UI-HF-BNO-alk-h-12-0-UI.rl NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079943 5', mRNA sequence.
AWS04644
AWS04644.1 GI:7142311
EST
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/db_xref="taxon:9606"
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/cell_type="MGGB (LT1)"
/cell_type="mgGB (LT1)"
/cost-"wcted from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
84 a 72 c 126 9 9 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotan Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia: Eutheria: Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 420)
NIH-MGC http://mqc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
ECO RI site shown at the beginning of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: M.G. clone distribution: M.G. clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image.html
Seq primer: MI3 Forward
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                                                                                                                             Score 15; DB 10;
Pred. No. 5.6e+02;
0; Mismatches 0;
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                                   91
      TAG_SEQ=AATGC"
                                                                                                                             100.0%;
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                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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//lab_host="taxon:97:320-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NCI_CGAP_Sub1 library, which is a subtracted library
derived from BI. BI constitutes a mixture of 21
normalized or subtracted NCI_CGAP_IDARY, which is a subtracted library
derived from BI. BI constitutes a mixture of 21
nOTI_CGAP_LOIG NCI_CGAP_F128, NCI_CGAP_CO10,
NCI_CGAP_EDAZ; NCI_CGAP_ROS, NCI_CGAP_LUNC;
NCI_CGAP_EDAZ; NCI_CGAP_ROS, NCI_CGAP_LUNC;
NCI_CGAP_EDAZ; NCI_CGAP_ROS, NCI_CGAP_LUNC;
NCI_CGAP_EDAZ; NCI_CGAP_GC4, NCI_CGAP_LUNC;
NCI_CGAP_LUNG; NCI_CGAP_LOS, NCI_CGAP_LUNC;
NCI_CGAP_EDAZ; NCI_CGAP_LOS, NCI_CGAP_LUNC;
NCI_CGAP_LUNG; NCI_CGAP_LOS, NCI_CGAP_LUNC;
NCI_CGAP_ROS; These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 LLAM 3337, 3682-3683;
150052-1502855; NCI_CGAP_Kid5 pool 1 LLAM 3364-3379;
1720-3725, 3776-3778 (IMAGE CloneIDS 1232911, 1456008-1456775
1720-3725, 3776-3778 (IMAGE CloneIDS 12414920-141991, 152091-152249); NCI_CGAP_Kid5 pool 1 LLAM 3575-358; 3881-3854 (IMAGE CloneIDS 1257096-1258631, 1479904-132404, 1453255); NCI_CGAP_FDACON 1 LLAM 3575-358; 3881-3854 (IMAGE CloneIDS 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI_CGAP_PDACON 1 LLAM 267-2453, 2786-2759, 3062-3068 (IMAGE CloneIDS 12706-1258631, 1540966-1528681, 1010120-11 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDS 1057096-1258631, 1010120-11 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDS 10574094-1443351); NCI_CGAP_CON POOL 1 LLAM 2659-2708-2708-2708
                                                                                                             UI-H-BIL-aeb-a-03-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone AMI39708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Emal: cgapbs-remail.nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
1s likely internal to the message cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
Information can be found through the I.M.A. G.E. Consortium/ILNL at:
www.bio.linl.gov/bbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 151-216, >(GGGA
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 410)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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TAG_TISSUE=kidney
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                                                                                                                                                                                                                                                                                AW139708.1 GI:6144426
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Unpublished (1997)
114 CCTTCTCCCCCTGTT 100
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source

FEATURES

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Gaps

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Best Local Similarity 100.
Matches 15; Conservative
         130 CCTTCTCCCCTGTT 116
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The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
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                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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www.bio.llnl.gov/bbrp/image/image.html
Seq primer: Ml3 Forward
POLYATES.
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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TAG_TISSUE=brain
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1 (bases 1 to 430)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
BG961625 410401-007-C09 CT0642 Homo sapiens CDNA, mRNA sequence.
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Fax: +55-11-2707001
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-CTO&42-240401-007-C09&t3=2001-04-24&t4=1)
Seq primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                         Hertzberg,M., Aspeborg,H., Erlandsson,R., Bjorkbacka,H., Hiltonen
'T., Karlsson,J., Teeri,T., Gustafsson,P., Bahlerao,R., Jansson,S.,
Nilsson,O., Sundberg,B., Nilsson,P., Uhlen,M., Sandberg,G. and
Lundeberg,J.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-
211100-494-c07&t3=2000-11-21&t4=1)
Seq primer: puc 18 forward
EST.

Populus balsamifera subsp. trichocarpa.

Populus balsamifera subsp. trichocarpa

Populus balsamifera subsp. trichocarpa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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//db_xref="taxon:3694"
//clone_lib="Populus flower cDNA library"
/note="Organ: flower"
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Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
Tel: 46 B 790 8287
Fax: 46 B 245452
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100.0%; Pred. No. 5.6e+02;
iive 0; Mismatches 0;
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Unpublished (2001)
Contact: Erlandsson R
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                                              /organism="Homo sapiens"
High quality sequence start: 12
High quality sequence stop: 29.
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM nucleic - nu	OM nucleic - nucleic search, using sw model	
Run on:	December 11, 2002, 12:26:07; Search time 1657 Seconds (without alignments) 263.453 Million cell updates/sec	
Title:	us-09-750-609-10	
Periect score: Sequence:	15 1 octtotococctgtt 15	
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Maximum Match 100% Listing first 45 summaries GenEmbl:* Database :

em_htg_hum:*
em_htg_inv:*
em_htg_other:* 9b ba: *
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

HSA288489 190 bp DNA linear PRI 04-APR-2001 Homo sapiens partial COL4A3 gene for alpha3 type IV collagen, exon Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 190)

Heidet, L., Arrondel, C., Forestier, L., Cohen-Solal, L., Mollet, G., Gutierrez, B., Stavrou, C., Gubler, M.C. and Antignac, C. AJ288489 AJ288489.1 GI:13559182 alpha3 type IV collagen; col4a3 gene. human. RESULT 1 HSA288489/C LOCUS DEFINITION F ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

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Sksdiookddssivpwllsfrrgtaleeggnkiviketgyffiygovlytdtframgh
Liorkkahvrgddlslvylfrcionmposypnnscytagiakleegdbloliiprrra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the TNF family
Structure of the human type IV collagen gene COL4A3 and mutations in autosomal Alport syndrome J. Am. Soc. Nephrol. 12 (1), 97-106 (2001)
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Schneider,K., Kolthow,S., Schneider,P., Goebel,T., Kaspers,B. and
                                                                                             Direct Submission
Submitted (28-MAR-2000) Antignac C., U423, INSERM, Hopital
Necker-Enfants malades 149 rue de Sevres, 75015 Paris, FRANCE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus TNF family B cell activation factor (BAFF) mRNA, AF506010.1 GI:22087370
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Schneider K., Kolthow, S., Schneider, P., Goebel, T., Kaspers, B.
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Submitted (24-APR-2002) Virology, University of Freiburg,
                                                                                                                                                                                                                                                                                                                                                                              0;
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/protein_id="AaM90951.1"
/db_xref="GI:22087371"
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Antignac, C.
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'S Isogai, T. and Otsuki, T.

Direct Submission

**Laboratory: 1532-3 Yana, Kisarazu, Chiba 20-0812, Japan

**Laboratory: 1532-3 Yana, Kisarazu, Chiba 29-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association, for Biotechnology; cDNA full insert construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

**Location/Qualifiers**

Irce //organism="Homo sapiens"

// **Laboratory of Tokyo.**

// **Comparism="Homo sapiens"

// **Laboratory of Tokyo.**

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/db_xref=nG1:10433147"
/db_xref=nG1:1043147"
/db
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1689 bp mRNA linear PRI 01-AUG-2002
Homo sapiens cDNA FLJ11805 fis, clone HEMBA1006278, moderately
similar to POLY(A) POLYMERASE (EC 2.7.7.19).
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AK021867.1 GI:10433146

Oligo capping; fis (full insert sequence).

Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA

mRNA, clone_lib:HEMBA1 clone:HEMBA1006278.
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186. >1689
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100.0%; Pred. No. 1.2e+03;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3190)
                                                                                                            Direct Submission
Submitted (15-000-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                            CDNA Library Preparation: Rubin Laboratory
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                                                                                                                                                                                                  AF232676 1721 bp mRNA linear MAM 22-NOV-2000 Sus scrofa prophet of pit-1 (Prop-1) mRNA, complete cds. AF232676.1 GI:11275672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (07-FEB-2000) Biology, Indiana University Purdue
University Indianapolis, 723 West Michigan Street, Indianapolis, IN
46202-5132, USA
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/protein_id="AAG3702.1"

/db_xref="G1:11275673"

/translation="MEAEGRREGGKPRKGRVCSSLWPEGYPAAGTLTARVDISTRPYR

NLSGWGAGRPRLSPRENRIFTFFFBAGLEGLESAPGRNVDEJSTRPYR

ALSGWGAGRPRISPRENRIFTFFFBAGLEGLESAPGRNVDPINAREGL

ARDTGLESATIQWWFORRAKGRYGBRSLLOPLAHLSPATFGGFLPEPPACPYSYPTP

PPPMTCFPHPYNHALPSQPSTGGSFARHPQSEDWYPTLHPTPTGHLPCPPAPPVLPLS
                                      ó:
                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1721)
Sloop, K.W., McCutchan Schiller, A., Smith, T.P., Blanton, J.R. Jr.,
Rohrer, G.A., Meier, B.C. and Rhodes, S.J.
Blochemical and genetic characterization of the porcine Prophet of
Pit-1 pituitary transcription factor
Mol. Cell. Endocrinol. 168 (1-2), 77-87 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1721)
McCutchan Schiller, A.L., Sloop, K.W., Blanton, J.R. Jr., Meier, B.C.
                                        Gaps
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100.0%; Score 15; DB 9; Length 1689; 100.0%; Pred. No. 1.1e+03;
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1larity 100.0%; Pred. No. 1.1e+03;
Conservative 0; Mismatches 0;
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                                    0; Mismatches
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/db_xref="taxon:9823"
1. .1721
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1. .1721
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                                                                                           123 CCTTCTCCCCTGTT 109
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                                                                      1 CCTTCTCCCCTGTT 15
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Matches 15; Conserv
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 7 Row: 1 Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTGTWYORWGVRALSLGGGOWGNFLSCFGPEYRRITLMMAGVWFTWSFSYYGLTTWFP
DMIRHLQAVDYASRTKVFPGERVEHVTFNFTLENQIHRGGOYFNDKFIGLRLKSVSFE
DSLFEECYFEDYVFSNTFFRNCTFINNVFYNPDLFEYKFWNSRLINSFFLHKEGCPL
DVTGFGARMYFVSFLGTLAVLFGUNIVSALLMDKIGRIRMLAGSSVMSCVSCFFLS
FGNSESAMAALLCLEGGSVSIASWMALDVLTVELY PSDKFRTAFGFLNALCKLAAVLGI
SIFTSFYGITKAAPILFASAALAGSSLALKLPETRGOVLO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="Similar to KIAA0736 gene product"
/product="Similar to KIAA0736 gene product"
/product="A="AAH00776.1"
/production_le" aAH000776.1"
/db_xrof="GI:12653963"
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OPESPRFFLENGKHDEAWMVLKQVHDTNMRAKGHPERVFSVTHIKTHQEDELIEIQS
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                                                                                                  contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3509807"
/tissue_type="Brain, neuroblastoma"
/clone_lib="NIH_MGC_19"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pOTB7"
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/translation="NKEMBANTVLDSQRQQKHYGITSPISLASPKEIDHIYTQKLIDA
MKPPGVFEDEBELNHRLVVLGKLNNLVKEWISDVSESKNLPPSVVATVGGKIFFGGSY
RLGYHTRGADIDALDARHYERSDFRQSFFERLKHQDGIRNLRANDDAFVPUT KFEF
DGIEIDLVRARLATOTISDNLDLRDDSRLRSLDIRCIRSLNGCRVTDEILHLVPNKET
FRLTLRAVKLWAKRRGITSNNLGFLGGVSWAMIVARTOCLYPRAAASTIVHKFFLVFS
KWEWPRDPVLLKQPEESNLINLPWNDPRYNPSDRYHLMPI ITTPAYPQONSTYNVSTSTRT
VMVEEFKQGLAYTDEILQGKSDWSKLLEPPPRFQKYFHYI VLITASASTERBHHEDWYGL
VESK TRVLVGNLERREFITLAHVNPQSFPGKKEHHKDNNYSBWFLGIIFRRYENES
VNIDLTYDIQSFTDTVYRQANNINMLKEGMKIEATHVKKKQLHHYLPRAGIKKKKQS
LSDVNRSSGGLOSSRRLSLDSSCLDSSRPTDNOTPFRNSPASKSDSPSYGETERRNSAEPA
AVIYERPLSVPPAGGLSIPTQRKYDSTVRYYSPPTVCTIFTYVGRNVIPRITTPHNP
AQGOPHLNGMSNITKTVTPKRSHSPSIGGTFKRDVEKFILLESTFKRDFRTR
KSVDAGIGGESMPHTDTIDTSRKKRLPSFELDSSSSPVDANNIRVIKNSIRLLESTFRDRABERRR
KSVDAGIGGESMPHTDTIDTSRKKRLPSFELDSSSSPVDANNIRVIKNSIRLTINR"
                                                                                                                      Topalian, S.L., Gonzales, M.I., Wang, X. and Wang, R.-F. Direct Submission Submitted (09-OCT-2000) Surgery Branch, NCI, National Institutes of Health, Building 10, Room 2B47, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanaka,A., Kotani,H., Nowira,N. and Ohara,O.
Prediction of the coding sequences of unidentified human genes. XI.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
99087487.
                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to Homo sapiens poly(A) polymerase protein (PAP) encoded by GenBank Accession Number X76770" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens adult male brain cDNA to mRNA, clone_lib:pBluescriptII
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase, T., Ishikawa, K., Suyama, M., Kikuno, R., Miyajima, N.,
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Ohara,O., Suyama,M., Nagase,T., Ishikawa,K. and Kikuno,R.
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Homo sapiens mRNA for KIAA0736 protein, complete cds.
AB018279
                     Mol. Cell. Biol. 21 (16), 5614-5623 (2001) 21356984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="neo-poly(A) polymerase"
/protein_id="AAK83701.1"
/db_xref="GI:15080911"
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ilarity 100.0%; Pred. No. 1.1e+03;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/cell_type="malignant melanoma"
                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                    (bases 1 to 3752)
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SFTVLSGCASRGTTGLPQEVHVLNLRNPDEGLDHHEREVTLHLTPISSVHTHQKPLVF
LLNSPLPLVMKLKTEELAPGIRKVFFYSSGSIVWFEKGNFSLSARFTEEKRFPERRBHL
LQMAQKEYGAVTSRTELKISRNIYIRVGEDGVFPPTCNIEKNFISLNYLAGYLQPKRA
EGCLMSNLVQEREVHIELITPNSNPYSARQVOITVDIKFSQFGAKLERNWYLLLKCK
KSYNWYIKENPOVGKLEVITSNSIGFEKETERSMTMSKSVIPDIPSSHESLIKWAYEH
KYSPVTSYTKAPVANRFHLQLEHTEEMNDEEDHSLELHGAKNRALSIKANYEH
FHINRGGHFTGGEGIFPPRRDSVDTLINHDFEHSLSKHKEPEBVGGSADVALSIKODK
VMTVAVEKDSLQASGYTRTELSLLDHSCKARNNGTHFILESLPNKCGTRTSYILDKIV
VRNSIVIQUESSPREGSSFEDDDDMSSQDOMSFQDDAGSGTYPTFILESLPNKCGTRTSYILDKIV
                                                                                                                                                                                                          1 (bases I to 3347)
Barnett,J.V., Moustakas,A., Lin,W., Wang,X.F., Lin,H.Y.,
Barnett,J.V. Moustakas,A., Lin,W., Wang,X.F., Lin,H.Y.,
Caloning and developmental expression of the chick type II and type
III TGF beta receptors
Dev. Dyn. 199 (1), 12-27 (1994)
8167376
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LGFALQTCFVSPFSNPDRMSDYTIENICPRESSVRFSTEKLNFPLAHAQKDKRRFS
FVFKPIFNISLLFLHCELTLCTNIDKDTQRLPKCVPPDEACTSLNVDMILAMMHNKKT
FTKPVITHEGKPEDSSLPKSNVRQPSVFYGLDTLTVVGIAFAAFVIGALLTGALWFI
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Homo sapiens neo-poly(A) polymerase mRNA, complete cds.
AF312211
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                                                                        Gallus gallus (library: lambda zap) embryonic brain cDNA to mRNA. Gallus gallus gallus Bukaryota: Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata; Euteleostomi;
  TGF-beta; betaglycan; plasma membrane; transforming growth factor-beta receptor; transforming growth factor-beta type III
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Topalian, S.L., Kaneko, S., Gonzales, M.I., Bond, G.L., Ward, Y. and
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/product="transforming growth factor-beta type III
receptor"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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712 c 708 g 931 t
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152. .2677
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/db_xref="GI:511843"
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/dev_stage="embryonic"
/germline
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1 Similarity 100.0%; P:
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Best Local Similarity
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Length 3752; Indels PRI 16-JUN-1999

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.6848,7063. .7131,7228. .7342,7460. .7587,7693. .7787
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FDRAMTSILAKHLQELMDGLTAKVFRTYNASITLQQQLKELSGSDDSYPAKILSYNRA
NRAVAILCNHQRAPPKTFEKSMONLQTKIDEKOKQLSAARKQLKAAKAEHKASHDDKS
KRAVEVKRKAVQRIEDLMKLQYQATDREENKQIAGTSKLNYLDPRISVAWCKRFGI
PIEKIYNKTQREKFARAIDMAEKDFEF"
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                                                                                                                              /gene="toplalpha"
join(1812. 1844,2092. .2116,3187. .3283,3527. .3653,
4037. .4092.4204. .4308,4394. .4487,4572. .4654,4730.
4930. .5051,5125. .5247,5324. .5511,6159. .6303,6400.
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/gene="toplalpha"
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4204. .4308
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3284. .3526
/gene="toplalpha"
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/gene="toplalpha"
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/gene="toplalpha"
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4037. .4092,4204. .4308,4394. .4487,4572. .4654,4730. .4845,
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GREFOWTLYFUCGLALMADGYEVPCYGFULPSAERDMCLSDSRKGMLGLIVYLGAMYG
AFLWGGLADRLGFRQCLLISLSVNSVFFFSSFVQGYGTFLFCRLLSGVGIGGSIPIV
SYSTEBELLAGERRGELLESWLCMFWMCGYYAAAMANAITPHYGWSFQWGSAYQFHGWY
VFVLVCAFPSYFALGALTTQPESPRFFLENGKHDEAMYLKQYHDTUMRAKGHPERVF
SYTHIKTHQEDELLEIQSDTGWYQMRGYRALSLGGGVWGNFLSCFGPPYRRITLMM
MGVWFTWRSFSYYGLTWWFPDMIRHLQAVDYASRTKVPFGERVEHYTFNFTLENGTILMM
MGVWFTNGFSYYGLTWWFPDMIRHLQAVDYASRTKVPFGERVEHYTFNFTLENGTILMM
LIKALLAGESYWGCYSCFFESFGRAYWYFFOR SELGTLANTGENTYFLENGTLENYF
LIKALGGSYMGCYSCFFESFGRAYWYFFOR SELGTLANTGENTYFLENYFLENYFIC
TTAFGFELNARGGSYMGYGTGGERAWYFFYSFCTGTLANTGENYFTYEFSKF
TTAFGFELNARGGSSMIALLCFFGYSEGWIALGGSSLALKLPETRGCY
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SYSRFEEEDDDDDFPAPSDGYYRGEGTQDEEEGGASSDATEGHDEDDEIYEGEYQGIP
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Fugu rubripes cosmid 092H06 genomic DNA fragment, toplalpha gene.
AL035357
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1 (bases 1 to 1101)
Smith, S. F., Metcalfe, J. and Elgar, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (01-FEB-1999) Smith S.F., Fugu Group, UK HCMP Resource
Centre, Wellcome Genome Campus, Hinxton Hall, Hinxton,
Cambridgeshire, CB10 1SB, UNITED KINGDOM
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Takifugu rubripes.
Takifugu rubripes
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Best Local Similarity
Thes 15; Conserva
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FR092H06/c
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Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
1 (bases 1 to 11896)
Fitz-Gibbon, S.T., Ladner, H., Kim, U.J., Stetter, K.O., Simon, M.I. and
Miller, J.H.
                                                                                                                                                                                                                                                                                                             AE009810 11896 bp DNA linear BCT 16-JAN-2002
Pyrobaculum aerophilum strain IM2 section 65 of 201 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum
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Fitz-Gibbon, S.T., Ladner, H., Kim, U.-J., Stetter, K.O., Simon, M.I. and Miller, J.H.

Direct Submission
Submitsed (12-Dece 2001) Microbiology and Molecular Genetics, University of California, Los Angeles, 405 Hilgard Ave, Los Angeles, CA 90095-1489, USA
Angeles, CA 90095-1489, USA
I. 11896
/organism="Pyrobaculum aerophilum"
// Strain="IMA"
                                                                                                                                                                Gaps
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0
                                                                                                                              Length 11001;
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11792869
                                                                                                                                                                Indels
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Pred. No. 9.8e+02;
; Mismatches 0;
                                                                                3161 t
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AE009810 AE009441
AE009810.1 GI:18159943
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                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
                                                                                                                                                                                                                 6409 CCTTCTCCCCCTGTT 6395
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ORIGIN
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Complement(7231. .7931)
                                                        /note="DNA metabolism; DNA replication, recombination, and
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GNPVHSTPERAAAIARYIKEKGYRLGVKMAGGIRTREQAKAIVDAIGWGEDPARVRLG
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complement(8361, .8789)
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TFIRCIAGLETPTKGRILEGDAPVIDVERGINIPPAKRNVGMVFONWALYPHMKVFDN
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3779. 4897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEGAEMVAREHKMTREELDWVAYESHMRAWRATENKWFDDLEP I BGELGGVY VKLERD
BGI RPDTTHWRELAKLKRAFRDGVLTAFGNSSOLSDGAAVLLAWSEKRAREMGVKPTAR
I LCGY SWHMVEPWRFTEAPVYA I OKLIKKLGPE I DSEDYFEANBAFAVNUL VHRILGY
PYEKLNVFGGAI ALGHPLGASGARI VTTLI SVLRNKGGRRGI RALCHGTGGGTAIALE
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KEVEEVIFGSTLQGGMGQNLSRYAALLAGLPVEVSAYTVNRVCSSGMQAIIEAYREIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="G1:18159948"
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TSKEAYETGFGIDFGAYAVLAVPELEQYVLKGLERHYADAKRATEIVSSQRYKLITTG
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STVAAALAVEALGRQRVLGLLMPSLYTPPEDLKDALDVINALGVEWKRVDJTPIYDAF
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DPGAVAYIKSLFKEFVKSGLLKVLLAPAESLPPADGECDSVISVAAVHHFRDIEVALR
EMVRVAKRLVAIYDWTPEAGGVTNPHSPQELEAKMRAAADAAVKLGFDIKITRYWYRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="PAE1222"
/note="Transport and binding proteins; Unknown substrate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="ABC transporter ATP-binding protein, putative"
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/db_xref="GI:18159947"
                                                                                                                                                                                                                            note="Fatty acid and phospholipid metabolism;
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                                                                                                                                                                                                                                                                                                                                          /product="acetyl-CoA C-acetyltransferase"
/protein_id="AAL63334.1"
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                                                                                                              complement(1424. .2608)
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4887. .5378
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3779. .4897
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                                                                                                                                        /gene="PAE1220"
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3 (bases 1 to 12602)
Avalos-Ramirez,R., Orlich,M., Thiel,H.-J. and Becher,P.
Complete genomic sequences of pestiviruses from giraffe and
reindeer: evidence for the presence of two novel species within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Translation="MELIKFELLYKTSKQKPVGVEEPVYRRTGEPVFGEPSPIHPQAS"
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KKKCKVKSKSTADGLYHNKNKPEQSRKKLEKALLAWAILAVLFQPVAGENITOWNLSD
NGTSGIQHAMYLRGVNRSLHGIWPEKICTGIPTHLATDTELKRISGMMDASEETNYTC
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                                                                                                                                                                                                                                                                                                                                       pestivirus giraffe-1 H138.
pestivirus giraffe-1 H138
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                           ö
                                                                                                                                                                                                                                    VRL 23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetic diversity of pestiviruses: identification of novel groups and implications for classification Virology 262 (1), 64-71 (1999)
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-APR-1999) Justus-Liebig-Universitaet Giessen, Institut fuer Virologie (Fachbereich Veterinaermedizin), Frankfurter Str. 107, Giessen D-35392, Germany 5 (bases I to 12602) Avalos-Ramirez, R., Orlich, M. and Becher, P. Direct Submission
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Becher, P., Orlich, M., Kosmidou, A., Konig, M., Baroth, M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avalos-Ramirez, R., Orlich, M., Thiel, H.J. and Becher, P. Evidence for the presence of two novel pestivirus species Virology 286 (2), 456-465 (2001)
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    Length 11896;
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/specific_host="Giraffa camelopardalis"
/db_xref="taxon:119222"
                                                                                                                                                                                                                                    AF144617 12602 bp RNA
Pestivirus giraffe-1 H138 complete genome.
Score 15; DB 1; 1
Pred. No. 9.7e+02;
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                                           Mismatches
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100.0%; Pr
tive 0;
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Becher, P. and Orlich, M.
Direct Submission
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AF144617.2 GI:15282441
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                                                15; Conservative
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  Query Match
Best Local Similarity
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CRYGGETE PERSOGNED EARTH NA IF I READSMAIN TRANDARCH REPRAINE ENCY CUCCUSTOR PERSON CONTRIBUTED AND CONTRIBUTE IGSTWTSIGIKLEKLPVVRAQTDTTSFHDAIRDKIDKKENLONPTLHTKLKEIFNNLS RPELRETYDEVDWGELEIGINRKGAACFLEKKNIGEILTTEKKSVEEIIKKLROGRLI NYYETAIPKNEKRDVNDDWEAGDLVTEKKPRVIQYPEAKVRLAITKVWYKWVKQKPVV VSHRPEDIEFCSHTPVPVRWADHTSSYMAGRNTATILSKMATRLDSSGDRGTAAYEKA VAFSPLLMYSWNPLVRRLCLMVMSKTHEVQPNKQAIYCYEGDPIAAYRDVIGHNLYEL KRTGFEKLASLNLSMSVLGIWTKHTSKRLIQDCIEVGKGDGNQLVNADRLVSSKTGHI YVPGSGYVVQGRHYEELSITKRPDRQTSNGLERYNLGPIVNLVLRRLRVMLMASIGRG RKWHKFLDAITEHMTQVPVITADGEVYIREGQRGSGQPDTSAGNSMLNVLTMIYAFCE ö MKRGKAGYREYSEEPCNREGYEISTRCKLCIIEKTOWKVYAADNTLCPMPCKPMEII SSEGPVSKTACTFNYTETLENKYFEPRDEYFQOYMLKGKYOYWFDLKATDNRKDYFAE FLYLAVVALLGGRYUMLLYTFYTFOEASGLOLDEGVVWHIGNLITEDNIEWYVYF LLTLETVNREDPVKKWVICLYHCLTMKPIRTAAULVILMSNNVNGEGGSKAGAGIDLYF LTTLGWYVFLYLARFDPMLIPLYVAATATFKTTKYTAGFSVDYALAVLLIVLLICSYTS DYFKYRKLLQCLLSIGAAVFLIRSLKWLGGVGLPSIELPTQRPFYILVYLLIGTALVT SWNLDIAGSLIQAVPILLLIFTLMADILTLIUVLPTYELAKT IQGVVDFYYKGATIRVDTGNGKTVTATDKWEIDHATITRLLKKHTGIGFNGAYLGEEP NYKDLIGRDCATITRDSVQFLKMKRGCAFTYDLTLSNLVKLIELVHKNKLEEREIPEV TVTTWLAYVEVDEDVGTIKPCLGEKVIPEKTGDVSLQSEVILDTTSVGISVVGGSDRA TTGITPVVIEKQSVTGGNQNIIKIGLSEGEYFGFGVNRASISQAVEERUNRPWVLLLG SAIYLVLHYTMPQKYEVVGSCDRNQLNLTVKTRVEDVIPSSVWNIGKYVCVRPDWWPY ETTTVFIFEEVSQVVKLVLRALRDLTRIWNAASTTAFLICLVKVLRGQVIQGIVWLLL. VTGAQGAITCEPEXQYALARSKRIGPLGAEDLVTTWHDYKFDLKIQDPLVMVYCKNDQ RURYKRUTTYVDLEGSGEGVILPPSKMGGRDGFDFTLPLLRAVLISCVSSYWOTFYLM TALDDLLYVYHRKIIEEVAGGTULLASKLAALIELUWTVDSEBSKGLKRFFVLTSRVK NLVMKHKVRNDLVARWYEDEELYGMPKLVSTYRAASILSKTKGCILCTVCENKDWKGVN CPKGGGTGPPLSCGMTLADFERRHYKRIFIREDSMNTMMCNRCQGKHRRFEMDREPKS SDKATSNRVKTARNVRLYKGSDPVEVRRLMREGRLLVISLRDTDKGLHQYIDFKGTYL TRETLEALSMGTPKAKQITKAEVRELLSPPSEDSGLPDWLTAENPVFLEATIRQEKYH IVGDVDVVKTKAKELGATDDTKIVKEVGARTYTMKLSSWFTQQSNKHHSLLPLFEEVL LQCPPKNPNPRVHMVSAYQLAQGNWEPVDCGVHLGT1PAKRSKTHPYEAYTKLKELLE IPGYEGKTPLFLIFDKVKKEWDQFQDPVAVSFDTKAWDTQVTSRDLELIRDIQKYYFK STGVPYRSFNRVAKIHVCGDDGFLITEKSLGLKFASRGAQILHEAGKPQKILEGDRMK EHKNSNEMGCGMVKEHNKWILRKIKHHGNLRTKHILNPGKLSEQLARDGGKHNIYNKI FFVGKRCKAGEARYLAKIHWRALPTSVVFEKVLEENPPEELPLEDNFEFGLCPCDSRP VVKGNFNTTLINHSAFQLVCPIGWVGTIECTLVNTDTLATTVVKRYTRTTPFPMRAGC VVYKLIGEDLHHCTLGGNWTCVPEDDGTYTGGELEKCKWCGFKFRIPDGLPTYPIGRC Gaps 0; Length 12602; Indels E2 /product="structural glycoprotein 2545 c 3288 g 2716 t 100.0%; Score 15; DB 14; 100.0%; Pred. No. 9.7e+02; M. M. M. Preds 0; Best Local Similarity 100. Matches 15; Conservative 2447. 4053 a mat_peptide Query Match BASE COUNT ORIGIN

RESULT 12 BSSRFAP/c

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ELAGSGERFROISHFTUHVLSEQEYAQSRRFEKDRAWWROFESVPELVSLKRNASA
EGSLDAERFSKOVPRFLHQULLFCCRNKVYSLSVFQSLLAAYLXRVSGQNDVYTGTF
MGNRQNAKEKOMLGMFYSTVPLFTNIDGGQAFSEFVKDRMKDLMKTLRRQKYPYNLLI
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GRTAAVLCERSMDMIVSILAVLKSGSAYVPIDPEHPIQRWQHFRDSGAKVLLTQRKL
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VLVEQAIQEFIRRNDAMRLRLRLDENGEPVQYISEYRPVDIKHTDTTEDPNAIEFISQ
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EIDVDYSTKLFKQSTADRLLTHFARLLEDAAADPEKPISEYKLLSEEEAASQIQQFNP
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ANILRTVKETNYLSITEQDTILGLSNYVFDAFMFDMFGSLLNGAKLVLIPKETVLDMA
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2 (bases 1 to 32802)
Cosmina, P., Rodriguez, F., de Ferra, F., Grandi, G., Perego, M.
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                                                                                                                                                                                                                                             B.subtilis srfA-sfp gene region for surfactin synthetase. X70356 X70357 X70358 X70356 L GI:396480 surfactin synthetase. Bacillus subtit
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/strain="W168 derivative of JH642"
/db_xref="taxon:1423"
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/db_xref="GI:396481"
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                                            10231 CCTTCTCCCCCTGTT 10245
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Bacillus subtilis
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JOURNAL

TITLE

REFERENCE AUTHORS

REFERENCE

VGVTDNFFSLGGDSTKGIQMASRLNQHGWKLEMKDLNOHPTIEELTQYVERAEGKQAD GOPVEGEVILLPIQRWFFEKNFTNKHWNGSYWLHAKKGEPDEFUKEKTLQALIEHHDA LRWYKEGGEDVIQYNGGLEASAQLEVIQIEGQAADYEDRIEREAERLGSSIDLOEG GLLKAGLEQAEDGDHLLLAIHHLVVDGVSWRILLEDFSAVYTQLEQGNEPVLPQKTHS DTSSNPLFDAVFSMQNANIKDLTMKGIQLEPHPFERKTAKFDLTLTADETDGGLTFVL EYNTALFKQETIERWKQYWMELLDAVTGNPNQPLSSLSLYTETEKQALLEAWKGKALP VPTDKTVHQLFEETAQRHKDRPAVTYNGQSWTYGELNAKANRLARILMDGGISPDDRV GVLTKPSLEMSAAVLGVLKAGAAFVPIDPDYPDQRIEYILQDSGAKLLIKQEGISVPD SYTGDVILLDGSRTILSLPLDENDEBNPETRATABNIAZMYTYGGTGQPKGWW SYTGDVILLDGSRTILSLPLDENDENPETRATABNIAZWYTYGGPKGWW EHHALVNLCFWHHDAFSWATAEDRSAKYAGFGFDASIWEMFPTWSIGAELHVIEBAIRL DIVRLNDYFETWGYTITFLPTQLAEQFMELENTSLRVLTTGGBKLKRAYKKPYTLVNN YGPTENTVVATSAEIHPEEGSLSIGRAIANTRVYILGEGNQVQPEGVAGELCVAGRGL ARGYLNREDETAKRFVADPFVPGERMYRTGDLVKWTGGGIEYIGKIDQQVKVRGYRIE LSEIEVQLAQLSEVQDAAVTAVKDKGGNTAIAAYVTPESADIEALKSALKETLPDYMI PAFWVTLNELPVTANGKVDRKALNEPDIEAGSGEYKAPTTDMEELLAGIWQDVLGMSE KGKLLHMYGPSESTVFATYHPVDELEEHTLSVPIGKPVSNTEVYILDRTGHVQPAGIA HQVKIRGQAIELGEIEHQLQTHDRVQESVVLAVDQGAGDKLLCAYYVGEGDISSQEMR EHAAKDLPAYMVPAVFIQMDELPLTGNGKIDRRALPIPDANVSRGVSYVAPRNGTEQK LAQVIASAEKGTAASISPAEKQDTYPVSSPQKRMYVLQQLEDAQTSYNMPAVLRLTGE LDVERLNSVMQQLMQRHEALRTTFEIKDGETVQRIWEEAECEIAYFEAPEEFTERIVS **EFIKPFKIDQLPLFRIGLIKHSDTEQVLLFDMHHIISDGASVGVLIEELSKLYDGETL** EPLRIQYKDYAVWOHRFIQSELYKKQEEHWLKELDGELPVLTLPTDYSRPAVQTFEGD RIAFSLEAGKADALRRLAKETDSTLYMVLLASYSAFLSKICGQDDIIVGSPVAGRSQA DVSRVIGMFVNTLALRTYPKGEKTFADYLNEVKETALSAFDAQDYPLEDLIGNVQVQR FAEYAERLQDFANSKAFLKEKEYWSQLEEQAVAAKLPKDRESGDQRMKHTKTIEFSLT SRTVGWFTSMYPMVLDMKHADDLGYQLKQMKEDIRHVPNKGVGSGILRYLTAPEHKED VAFSIQPDVSFNYLGQFHQMSHPPFFTTSHLPSPHSLSPETEKPNALDVVGYIENGKL TMSLAYHSLEFHEKTVQTFSDSFKAHLLRIIEHCLSQDGTELTPSDLGDDDLTLDELD /translation="MSKKSIQKVYALTPMQEGMLYHAMLDPHSSSYSTQLELGIHAAF DLEIFEKSVNELIRSYDILRTVFVHQQLQKPRQVVLAERKTKVHYEDISHADENRQKE HIERYKQQVQRQAFNLAKDILFKVAVFRLAADQLYLAWSNHHIMMDGWSMGVLMKSLF QNYEALRAGRTPANGQGKPYSDYIKWLGKQDNEEAESYWSERLAGFEQPSVLPGRLPV YPGKTWTVK I KYNGAAFDSAFI ERTÄEHLTRMMEAAVDQPAAFVREYGLVGDEEQRQI VEVFNSTKAELPEGMAVHQVFEEQAKRTPASTAVVYEGTKLTYRELNAAANRLARKLV MIEHKSILRLVKNÄGYVPVTEEDAMAQTGAVSFDAGTFEVFGALLNGAALYPVKKRHV LDAKQFAAFLREQSITTWWLTSPLFNQLAAKDAGMFGTLRHLIIGGDALVPHIVSKVK QASPSLSLWNGYGPTENTTFSTSFLIDREYGGSIPIGKPIGNSTAYIMDEQQCLQPIG IDNQVKVRGFRIELGEIETKLNMAEHVTEAAVIIRKNKADENEICAYFTADREVAVSE LRKTLSQSLPDYMVPAHLIQMDSLPLTPNGKINKKELPAPQSEAVQPEYAAPKTESEK KLAEIWEGILGVKAGVTDNFFMIGGHSLKAMMMTAKIQEHFHKEVPIKVLFEKPTIQE EGEVDKDRLENAIQQLINRHEILRTSFDMIDGEVVQTVHKNISFHLEAAKGREEDAEE ADLELPQIHYKDYAVWHKEQTNYQKDEEYWLDVFKGELPILDLPADFERPAERSFAGE RVMFGLDKQITAQIKSLMAETDTTMYMFLLAAFNVLLSKYASQDDIIVGSPTAGRTHP VADIWAQVLQAEQVGAYDHFFDIGGHSLAGMKMPALVHQELGVELSLKDLFQSPTVEC **AEETEQLITKVHEAYHTEMNDILLTAFGLAMKEWTGQDRVSVHLEGHGREEIIEDLT** KKDEYVNKEYSFTWDETLVARIQQTANLHQVTGPNLFQAVLGIVLSKYNFTDDVIFGI VVSGRPSEINGIETMAGLFINTIPVRVKVERDRAFADIFTAVQQHAVEAERYDYVPLY EIQKRSALDGNLLNHLVAFENYPLDQELENGSMEDRLGFSIKVESAFEQTSFDFNLIV EHGLQKGETAAIMNDRSVETVVGMLAVLKAGAAYVPLDPALPGDRLRFMAEDSSVRMV LIGNSYTGQAHQLQVPVLTLDIGFEESEAADNLNLPSAPSDLAYIMYTSGSTGKPKGV APGELCVGGIGVARGYVNLPELTEKQFLEDPFRPGERIYRTGDLARWLPDGNIEFLGF LALYLEENESKEEQTFEPIRQASYQQHYPVSPAQRRMYILNQLGQANTSYNVPAVLLI IIKAFVQPFELNRAPLVRSKLVQLEEKRHLLLIDMHHIITDGSSTGILIGDLAKIYQG DLQGVPGMFVNTGALRTAPAGDKTFAQFLEEVKTASLQAFEHQSYPLEELIEKLPLTR DTSRSPLFSVMFUMQNMEIPSLRLGDLKISSYSMLHHVAKFULSLEAVEREEDIGLSF EATFAALFEKQAQQTPDHSAVKAGGNLLTYRELDEQANQLAHHLRAQGAGNEDIVAIV EGIIVSLDDGKWRNESKERPSSISGSRNLAYVIYTSGTTGKPKGVQIEHRNLTNYVSW FSEEAGLITKRRADGNDKTVLLSSYAFDLGYTCMFPVLLGGGELHIVQKETYTAPDEIA HYIKEHGITYIKLTPSLFHTIVNTASFAFDANFESLRLIVLGGEKIIPTDVIAFRKMY DYATALFKDETIRRWSRHFVNIIKAAAANPNVRLSDVDLLSSAETAALLEERHMTQIT MDRSAEVMVSILGVMKAGAAFLPIDPDTPGERIRYSLEDSGAKFAVVNERNMTAIGQ! /db_xref="SWISS-PROT:Q04747" /protein_id="CAA49817.1" /db_xref="G1:396482" /transl_table=11 /codon_start=1 .21543 10780. .21543 /gene="srfA2" /gene="srfA2" 10780. .21543 KLMEIF" 10780.

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GPTBNYVAPRTSÆLHPEEGSLSLGRA LANTRY VILGEGNGVPEGVAGESLCYAGKGLA,
RGYLNREDETARRPYADPFVPGERMY RTGDLVWWNNG IEX IGKIDQQVKNRGYRIEL
SEIEVQLAQLSEVEDRAVTRVKDKGGNTA IAAAYVTPETADIEALKSTLKETLEPDYMIP
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GVTDNFFSLGGDSIKGIQMASRLNOHGWKLEMKDLFOHPTIEELTOYVERAEGKQADO
GPVEGEVILTPIQRWFFEKNFTNKHHWNGSVMLHAKGFDPERVEKTLQALIEHDAL
RMVRREENGDIVQVYKPIGESKYSFETVDLYGSDEEMLRSQIKLLANKLQSSLDLRNG
PLLKAAESYRTEAGDHLLIAVHHLVVDGVSWRILLEDFASGYMQAEKEESLVFPQKTNS
                                                        LRYQLSLTLPSHMIPAFFYQVDAIPLTANGKTDRNALPKPNAAQSGGKALAAPETALE
ESLCRIWQKTLGIEAIGIDDNFFDLGGHSLKGMMLIANIQAELEKSVPLKALFEQPTV
RQLAAYMEASAVSGGHQVLKPADKQDMYPLSSAQKRWYVLNQLDRQTISYNMPSVLLM
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STYGWRTAGVEYULDISDANDANJVIKTWKENIENIEN IPDKGVGYGTILKFTFATEKTGFT
PEISFWYLGGFDSEWYKTDFFEPSAFDWGRQVSGESEALYALSFSGMINGRFYLSCSY
NEKEFERATVEEEMERFKENILLMLIRHCTEKEDKEFTPSDFSAEDLEMDEMGDIFFDML
RADDQVKIRGYRIELGEIETVMLSLSGIQEAVVLAVSEGGLQELCAYYTSDQDIEKAE
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LRIMGPGKLINCYGPTEGTVFATAHVVHDLPDSISSLPIGKPISNASVYILNEQSQLQ
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Gaps
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100.0%; Score 15; DB 1; Length 32802; 100.0%; Pred. No. 9e+02; ive 0; Mismatches 0; Indels 0
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                                 Conservative
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Query Match
Best Local Similarity
Matches 15; Conser
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RESULT 13 AC107069/c

PRI 29-MAY-2002 Submitted (29-MAY-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Apr 13, 2002 this sequence version replaced 9::19924179. Materston, R. H.
Direct Submission
Submitted (15-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 34578) Direct Submission Submitted (13-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MD 63108, USA 6 (bases 1 to 34578) Sequencing Center, Washington 4444 Forest Park Parkway, St. Louis, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 34578) Sulston,J.E. and Waterston,R. AC107069 34578 bp DNA linear PRI 29-M Homo sapiens BAC clone RP11-249A8 from 2, complete sequence. AC107069 Center: Washington University Genome Sequencing Center 2 (bases 1 to 34578) Scott.K., Kozlowicz,A., Spalding,L. and Trani,L. The sequence of Homo sapiens BAC clone RP11-249A8 3 (bases 1 to 34578) Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998) Center project name: H_NHO249A08 Direct Submission Submitted (04-ARR-2002) Genome University School of Medicine, MO 63108, USA 5 (bases I to 34578) ---- Genome Center AC107069.5 GI:20146820 code: WUGSC (bases 1 to 34578) Direct Submission Waterston, R.H. Waterston, R.H. Homo sapiens. Homo sapiens Waterston, R. Center 99063792 9847074 LOCUS DEFINITION ACCESSION ORGANISM AUTHORS TITLE TITLE JOURNAL TITLE JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS VERSION KEYWORDS JOURNAL JOURNAL REFERENCE AUTHORS MEDLINE PUBMED REFERENCE REFERENCE AUTHORS REFERENCE AUTHORS JOURNAL JOURNAL TITLE COMMENT SOURCE

this NOTICE: This sequence may not represent the entire insert of this colone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted: restriction digest.

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc MAPPING INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male SOURCE INFORMATION:

repeat_region

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donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong VECTOR: pBACCe3.6
                                                                                                                                          NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-495023, 2000 bp overlap;
the clone sequenced to the right is RP11-563C6, 2000 bp overlap.
Actual start of this clone is at base position 126621 of
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3071. .3357
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5637. .5789
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Best Local Similarity 100.0%;
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KEYWORDS
SOURCE
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                                                                                   http://www.sanger.ac.uk/Projects/C-legans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
RPI-310P17 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: porPACZ
IMPORTANT: This sequence is not the entire insert of clone RPI-310P17 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RPI-310P17 is at 1 in this sequence. The true left end of clone RPI-310P17 is at 4,3244 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                              The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1924. .2090 "note="LIMBB repeat: matches 6005. .6171 of consensus"
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note="LlMB8 repeat: matches 5147. .5429 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      879. .3641
'note="LTR17 repeat: matches 1. .780 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(428..891)
/note="match: GSS: Em:B53078"
/note="match: GSS: Em:B53078"
/note="match: GSS: Em:AQ269829"
/note="match: GSS: Em:AQ269829"
/note="match: GSS: Em:AQ269829"
                   Chordata; Craniata; Vertebrata; Eutele
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .5991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .295 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2151. .2266
/note="LIMB8 repeat: matches 5874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132. .426
/note="AluSq repeat: matches 1.
complement(428. .891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="match: GSS: Em:AQ112069"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1063. .4518
/note="match: GSS: Em:AQ508138"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4129. .4662)
/note="match: GSS: Em:AQ316392"

    43347
    organism="Homo sapiens"
    db_xref="taxon:9606"

                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP1-310P17"
/clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="6"
                                                      (bases 1 to 43347)
                                                                                                                                                                                                                                                                                                                                                                                                  eature key
                                                                            Tromans, A.
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ORGANISM
                                                      REFERENCE
AUTHORS
                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                       COMMENT
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/note="Alugy x repeat: matches 71. .308 of consensus" 1573. .15790
/note="Alugy x repeat: matches 1. .152 of consensus" 1582. .16108
/note="LiphAl6 repeat: matches 5830. .6110 of consensus" 16106. .16416
/note="LiphAl6 repeat: matches 1. .313 of consensus" 1647. .17711
/note="LiphAl6 repeat: matches 4517. .5830 of consensus" 1773. .18032
/note="LiphAl6 repeat: matches 7. .314 of consensus" 17737. .18032
/note="LiphAl6 repeat: matches 4125. .4510 of consensus" 18427. .18706
/note="LiphAl6 repeat: matches 3826. .4124 of consensus" 18703. .19271
/note="LiphAl6 repeat: matches 5774. .5331 of consensus" 18703. .19271 20944. .21113 20944. .21113 /note="AluSg/x repeat: matches 129. .299 of consensus" 21140. .21264 21/4). .21030 /note="LIMD3 repeat: matches 7476. .7579 of consensus" complement(21823. .22281) /note="16 copies 2 mer ac 100% conserved" /note="1558 / note="1558 / note="HERVL repeat: matches 1757. .1969 of consensus" /12998. .13299 .5956 of consensus" /note="AluSq/x repeat: matches 1. .133 of consensus" 5732. .7036 19949. .20211 /note="L2 repeat: matches 1194. .1452 of consensus" 20944. .21113 /note="AluS repeat: matches 152, .170 of consensus" 15499. .15731 .2750 of consensus" "AluY repeat: matches 168. .311 of consensus" .11158 'note="L2 repeat: matches 2290. .2750 of consensus" .2147 of consensus" .282 of consensus" 'note="AluSp repeat: matches 1. .305 of consensus" 3265. 8544 /note="AluJo repeat: matches 2. 289 of consensus" 'note="AluSc repeat: matches 1. .125 of consensus" 9893. 19948 note="MADE1 repeat: matches 5. .80 of consensus" .143 of consensus" 8711. 8799 /note="MIR repeat: matches 59. 145 of consensus" .208 of consensus" //note="35 copies 2 mer tt 68% conserved"
21747. .21896 19272. 19892 . /note="L2 repeat: matches 1452. /note="L2 repeat: matches 2580. 6304. .6577 'note="AluSx repeat: matches 9. "match: GSS: Em:AQ484379" .5178 7969. 8079 /note="MIR repeat: matches 28. 8265. 8544 'note="match: GSS: 21581. .21650 11255. .11286 9753. .9893 'note="AluY .0697.

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where oil retrieves are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEP: Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/HGP/Chr10
RP11-17G2 is from the library RPCI-11.1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMPORTANT: This sequence is not the entire insert of clone RP11-1762 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-1762 is at 56701 in this sequence. The true right end of clone RP11-397115 is at 2000 in this
                                humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On or before Jul 12, 2001 this sequence version replaced gi:7381811, gi:13396759.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1266. 1301

/note="L2 repeat: matches 2580. .2615 of consensus"

1305. .1352

/note="24 copies 2 mer ga 75% conserved"

complement(2038. .2454)

/note="match: GSS: Em:AQ358591"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L2 repeat: matches 2645. .2749 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .240 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MER1B repeat: matches 1. .285 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MER91A repeat: matches 5. .95 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match: GSS: Em:AQ812738"
2586. 2791
//note="MIR repeat: matches 45. .258 of consensus"
2799. 3119
//note="MIR repeat: matches 61. .212 of consensus"
complement(3478. .3937)
//note="match: GSS: Em:AQ475942"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6293. .6521 ._______ matches 9. .334 of consensus /note="MIR repeat: matches 9. .234 of consensus" 8688. .8929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .218 of
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/note="MER20 repeat: matches 103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5477. .5644
/note="MLT11 repeat: matches 68.
complement(5738. .6110)
/note="match: STS: Em:G53244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. 56701
Cyganism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         match: GSS: Em:AQ083388"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-17G2"
/clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .4317
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                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.00ce="Limcorrections" | 7.39 of consensus" | 7.8938 | 7.3902 | 7.00ce="Limcorrections" | 7.39 of consensus" | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 | 7.3938 |
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Human DNA sequence from clone RPI1-17G2 on chromosome 10, complete
                                                                                                                                                                                                                                                        / Layer. 123063

/ Layer. 123063

23148. .23417

/ Anote="LTR22 repeat: matches 38. .312 of consensus"

/ Anote="L2 repeat: matches 2005. .2146 of consensus"

/ Anote="L2 repeat: matches 61. .243 of consensus"

/ Anote="MIR repeat: matches 61. .243 of consensus"

/ Anote="Limber repeat: matches 281. .1953 of consensus"

/ Anote="Limber repeat: matches 281. .1953 of consensus"

/ Anote="Limber repeat: matches 2151. .3045 of consensus"

/ Anote="Limber repeat: matches 2151. .3045 of consensus"

/ Anote="Limber repeat: matches 2151. .3045 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chapman,J.
Direct Submission
Submitted (03-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
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                                                                                             22608. .22697
/note="L2 repeat: matches 2620. .2710 of consensus"
22829. .22868
/note="20 copies 2 mer aa 80% conserved"
22998. .23085
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/note="MER9 repeat: matches 1. .511 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(26913. .27340)
// note="match: GSS: Em:AQ225006"
28135. .28460
//note="WER7A repeat: matches 4. .346 of consensus"
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100.0%; Pred. No. 8.8e+02;
tive 0; Mismatches 0;
                            22304, .22755
/note="match: GSS: Em:AQ357726"
'note="match: GSS: Em:AQ714858"
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/note="MIR repeat: matches 6.
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AL583852 AC011691
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                                                                                                .568 of consensus"
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29356, .29488
/note="MER5A repeat: matches 50, .184 of consensus"
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8697. .28879
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29578. .29664
// note="WIR repeat: matches 82. .175 of consensus"
31386. .31508
31386. .31508
// note="MIR repeat: matches 42. .164 of consensus"
31974. .32354
// note="MLT11 repeat: matches 1. .410 of consensus"
32596. .33013
// note="MLT14 repeat: matches 128. .547 of consensus"
31807. .33823
// note="MLT14 repeat: matches 128. .547 of consensus"
31813. .34015
// note="MIR repeat: matches 50. .251 of consensus"
318122. .34214
// note="MIR repeat: matches 46. .140 of consensus"
35180. .35474
// note="MIR repeat: matches 46. .140 of consensus"
37028. .37195
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37274..37413

37274..37413

37274..37413

700te="L2 repeat: matches 2137..2276 of consensus"

77801..38047.

700te="L2 repeat: matches 2469..2750 of consensus"

3841..39465

700te="L2 repeat: matches 1655..2599 of consensus"

700te="L2 repeat: matches 59..220 of consensus"

700te="L2 repeat: matches 2517..2691 of consensus"

7102..41277

700te="L2 repeat: matches 55..462 of consensus"

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Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine;
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11-JAN-2000; 2000US-0175456.
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Compugen Ltd
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ABV50337
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The present sequence represents a probe for the A457P variant allele of a human norepinephrine transporter gene. The specification a method for susceptibility to sub-optimal norepinephrine transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter gene are useful for gene therapy for modulating norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, in humans the subject or occaine or contine or interest of the properties of the properties of the properties of the subject in the subject of the subject in the subject of the subject is in humans and animals such as mental illness, in humans and animals such as mental illness, in human and such as such as the subject or occaine or or other relevant diseases, psycho stimulant abuse e.g. cocaine or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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  particularly orthostatic intolerance in a subject by detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 15; DB 22;
100.0%; Pred. No. 4.1e+02;
ive 0; Mismatches 0;
                     polymorphism of norepinephrine transporter gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein 5' EST, SEQ ID NO: 13316.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID 13316; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 BP; 0 A; 8 C; 1 G; 6 T; 0 other;
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                                                            Claim 15; Page 69; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC09241 standard; cDNA; 352 BP
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                                                                                                                                                                                                                                                                                                                                                                                                    amphetamine abuse.
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length CDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate call carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                               Gaps
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                                                                                                                                                         Sequence 352 BP; 111 A; 73 C; 97 G; 69 T; 2 other;
                                                                                                                                                                                                                             0;
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Pred. No. 4.3e+02;
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                                                                                                                         expression and secretion vectors.
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-2001
                                                                                                                                                                                                                                                                                      AAH04051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ota T,
                                                                                                                                                                                                              RESULT 5
AAH04051/
x os
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of indentifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in claspnostics, forensics, gene mapping, identification of mutations in responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
           (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                     0;
                                                                                     Length 445;
                                                                                                                   Indels
                                             Sequence 445 BP; 109 A; 118 C; 109 G; 107 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #1856.
                                                                                 DB 23;
4.3e+02;
                                                                                                                   0
                                                                               Score 15; DB
Pred. No. 4.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 1856; 103pp; English.
                                                                                                                                                                                                                                                                                  AAS66052 standard; cDNA; 549 BP.
                                                                                                                   ó
                                                                                 100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                      13-FEB-2002 (first entry)
                                                                       Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                      370 CCTTCTCCCCTGTT 384
                                                                                                                                                         1 CCTTCTCCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABG01865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2001,
                                                                                                                                                                                                                                                                                                                      AAS66052;
                                                                                                                                                                                                                                                RESULT 4
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                                                                                                                                                                                                                                                                                                                                                   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito K, Yamamoto J;
Otsuki T;
                                                                  ;
                                 Length 549;
                                                                  Indels
Sequence 549 BP; 114 A; 178 C; 140 G; 117 T; 0 other;
                               100.0%; Score 15; DB 23; 100.0%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID 886; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                    Human cDNA clone (5'-primer) SEQ ID NO:886.
                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                  BP.
                                                                ;
                                                                                                                                                                                                 1051/c
AAH04051 standard; cDNA; 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-0300253.
2000JP-0118776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000JP-0183767
2000JP-0241899
                                                                                                                                                                                                                                                                                 26-JUN-2001 (first entry)
                                                                  Conservative
                                                                                                               423 CCTTCTCCCCCTGTT 437
                                                                                               1 CCTTCTCCCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-318749/34.
                             Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               full-length cDNAs
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Gaps

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Indels

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of 11gonucleotide comprision a sequence complementary to the 5602 nucleotide comprising a sequence complementary to the oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence of polynucleotide which comprises a 3'-end sequence of polynucleotide comprises a 1'-end sequence, where the comprises of least 15 nucleotides and the combination of the 5'-end sequence, and sequence is selected from those defined in the 5'-end sequence, and sequence is selected from those defined in c. the specification. The primer sets can be used in antisense therapy and congent of the primer sets can be used in antisense therapy and particularly full-length cDNAs. The primers are also useful for the cetter and/or diagnosis of the abnormality of the proteins encoded by the full-length without any specialised methods. AAH33632 and AAH33632 to AAH3672 represent human amino acid sequences; and AAH3629 to AAH3632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                  Length 827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saito K, Y, Otsuki T;
                                          Sequence 827 BP; 264 A; 138 C; 199 G; 223 T; 3 other;
                                                                                                                          0;
                                                                              Query Match 100.0%; Score 15; DB 22; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID 13660; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hikawa T, Hayashi K, Sa
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA sequence SEQ ID NO:13660
                                                                                                                                                                                                                                                                                                     AAH15437 standard; cDNA; 1689 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ota T, Isogai T, Nishikawa T,
Ishii S, Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1999; 99JP-0248036.
27-ANG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001 (first entry)
  of the present invention.
                                                                                                                                                                                   123 CCTTCTCCCCTGTT 109
                                                                                                                                                              1 CCTTCTCCCCTGTT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                             AAH15437;
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AAH15437/C
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<u>ب</u>

Yamamoto

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represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for gene therapy for modulating norepline phrine transport in a target cell and treating susceptibility to impaired noreplinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, hypertension, heart disease, psychostimulant abuse e.g. cocaine or amphetamine abuse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a variant norepinephrine transporter. The specification a method for screening for susceptibility to sub-optimal norepinephrine (NE) transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter genes are useful
                                                                                                                                                                                                                                                                                                                                                                                                                    Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine; amphetamine abuse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a
                                                                                                                        Gaps
                                                                                                                      .;
0
                                                                                      Length 1689;
                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human norepinephrine transporter variant A457P.
                                                                                                                      Indels
                                                  Sequence 1689 BP; 555 A; 309 C; 366 G; 459 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "norepinephrine transporter"
                                                                                  100.0%; Score 15; DB 22;
100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 43; Page 104-108; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                             AAH28083 standard; cDNA; 1854
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2000US-0175456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-2000; 2000WO-US35491
                                                                                                                                                                                                                                                                                                                                              05-SEP-2001 (first entry)
                 of the present invention.
                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                       123 CCTTCTCCCCTGTT 109
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/*tag=
                                                                                                                                                        1 CCTTCTCCCCCTGTT 15
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P-PSDB; AAB84533.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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11-JAN-2000;
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 S X G G
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Sequence 1854 BP; 356 A; 555 C; 493 G; 450 T; 0 other;

AAH28087;

RESULT 8 AAH28087

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Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Albehimer's disease; AlDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; mayocardial infarction; wound healing; cell proliferation; skin aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     food additive; food preservative; gene therapy; gene; ss.
                                                                                                                                                                                                                                              DNA encoding novel central nervous system protein #308.
                                                                                                                               ABK43728 standard; cDNA; 2159 BP.
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2000US-0189874.
2000US-0190076.
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2000US-0205515.
2000US-0209467.
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2000US-0216647.
2000US-0216880.
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2000US-0220963
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2000US-0224519
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2000US-0225267
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                                                                                                                                                                                                         05-JUN-2002 (first entry)
                       1362 CCTTCTCCCCCTGTT 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-02174
2000US-02174
   1 CCTTCTCCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200155318-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7-MAR-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-2000
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                                                                                                                                                                    ABK43728;
                                                                                            RESULT
                                    a
                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a variant norepinephrine transporter. The specification a method for screening for susceptibility to sub-optimal norepinephrine (NE) transport in a subject. The method comprises to botaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the subject to susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter genes are useful for gene therapy for modulating norepinephrine transport in a target cell and treating susceptibility to impaired norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, hypertension, heart disease, psycho stimulant abuse e.g. cocaine or amphetamine abuse.
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                                                                                                                                                                                                                                                                                                                                                      Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene
                                        Gaps
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 Length 1854;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "norepinephrine transporter"
                                                                                                                                                                                                                                                                                                                   DNA encoding human norepinephrine transporter variant.
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100.0%; Score 15; DB 22; 100.0%; Pred. No. 4.4e+02;
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 43; Page 119-121; 133pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                   AAH28087 standard; cDNA; 1854 BP.
                                  0;
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Ouery Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           amphetamine abuse; ss.
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29-SEP-2000;
29-SEP-2000;
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29-SEP-2000;
02-OCT-2000;
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02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
20-0C
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25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
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17-NOV-2000;
17-NOV-2000;
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include cutchimmune diseases e.g. rheumatoid arthritis, hyperproliferative cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. corneal infection, gastrointestinal disorders e.g. dysphagia.

Cc e.g. corneal infection, gastrointestinal disorders e.g. dysphagia.

Cc e.g. corneal infection, gastrointestinal disorders e.g. dysphagia.

Cc and pitutery dwarfism, cancers and disorders e.g. disorders e.g. leukaemia, disorders e.g. nonallergic rhinitis, renal disorders e.g. respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.

Cc leukaemia, disorders involving neovascularisation e.g. malignancies, contextiding failure and blood related disorders e.g. myocardial

Cc respiratory disorders end blood related disorders e.g. myocardial

Cc infarction. The polypeptides can also be used to aid wound healing and epithenial organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
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2000US-0251988.
2000US-0256719.
2000US-0251479.
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2000US-0251989
             2000US-0249215
2000US-0249216
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2000US-0249218
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2000US-0249245
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2000US-0249297
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P-PSDB; AAU87398.
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Best Local Similarity
Matches 15; Conserv
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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01-DEC-2000;
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RESULT 10

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P-PSDB; ABB90065
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                                                                                                                                                                        Homo sapiens.
                                       24-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders
              ABL90474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The colymerase chain reaction (PCR) primers, oligomers, and for chromosome confidentifying expressed genes. (I) is useful in gene therapy techniques (c restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in c disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in c responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and c mino acid sequences chas64197-AAS94564 represent novel human c diagnostic coding sequences of the invention.

C diagnostic coding sequences of the invention contact from WIPO c at ftp. wipo.int/pub/published_pct_sequences.
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                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                        mutations
                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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                                                                                     DNA encoding novel human diagnostic protein #19092.
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          AAS83288 standard; cDNA; 2451 BP
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23-AUG-2000; 2000US-0649167.
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                                                            13-FEB-2002 (first entry)
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Matches 15; Conservative
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P-PSDB; ABG19101.
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                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
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                                                                                                                                                       Homo sapiens
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                                    AAS83288;
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AAS83288/c
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ID ABL9
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, altergies, autoimmune themolytic anaemia, autoimmune thyroiditis; diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myccardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
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                                                                      Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; SEQ ID NO 1036; 2081pp + Sequence Listing; English.
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Human polynucleotide SEQ ID NO 1036.
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nes 15; Conserv
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Central nervous system: CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; renel ileukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
                 DNA encoding novel central nervous system protein #584.
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2000US-0224518
2000US-0224519.
2000US-022513.
2000US-0225214.
2000US-0225267.
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2000US-0227009
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17 MAR 2000;
19 MAY 2000;
07 JUN 2000;
28 JUN 2000;
30 JUN 2000;
30 JUN 2000;
30 JUL 2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                      Homo sapiens.
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 05-JUN-2002
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2000US-0246611.
2000US-0246613.
2000US-0249207.
2000US-0249208.
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2000US-0249297.
2000US-0249299.
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2000US-0232398.
2000US-0232400.
2000US-0232401.
2000US-0233063.
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2000US-0234998
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2000US-0235834
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2000US-0232081
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13-0CT-2000;
20-0CT-2000;
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                                               14-SEP-2000;
14-SEP-2000;
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novel central nervous system protein. (1) and polypeptides (111) encoded by (11), are used to treat a medical conditions and in diagnoses of a pathological condition. Disorders which are diagnosed or treated include autolimnum diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. carediac arrest, cerebrovascular disorders e.g. cerebral ischaemia, andjogenesis, nervous system disorders e.g. cerebral ischaemia, andjogenesis, nervous system disorders e.g. cerebral ischaemia, andjogenesis, nervous system disorders e.g. Alzheimer's disease and andjodenesis, nervous system disorders e.g. dysphagia, cancer infection, gastrointestinal disorders e.g. dysphagia, denocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, denocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cente kiney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
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                                                                                                                                                                                                                                                                                                                                                                          invention describes an isolated nucleic acid molecule (I) encoding a
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antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                     New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives .
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                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 594; 837pp; English.
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                                                                                                                                                                                                                      Ruben SM;
                                     2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251856.
                                                                                                          2000US-0251869.
2000US-0251989.
2000US-0251990.
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Les 15; Conserv
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                                                     05-DEC-2000;
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AAA16618 to AAA16697 encode the human secreted proteins given in AAY94898 to AAY94980, isolated from human adult brain, adult thyroid, adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult placenta, adult testis, whole embryo, adult cartilage, kidney, adult placenta, adult testis, whole embryo, adult cartilage, kidney, adult bladder, cDNA libraties. The polymoleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. The polymoleotides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on Southern gels, and as chromosome markers or tags to identify chromosomes or to map gene positions. The proteins can be used in the the chromosome or to map gene positions. The proteins combined treatment of immune deficiency (SCID), as well as viral, bacterial, fungal and other infections. These infections include human immunodeficiency (IVI), hepselifications include human immunodeficiency (IVI), hepselifications on proteins can be used to treat autoimmune disorders such as connoictive tissue disease, multiple sclerosis, systemic lupus contractive tissue disease, multiple sclerosis, systemic lupus
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                             infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus; connective tissue disease; multiple sclerosis; erythematosis; rheumatoid arthritis; autoimmune pulmonary inflammation; asthma; Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis; insulin dependent diabetes mellitus; graft-versus-host-disease; autoimmune inflammatory eye disease; allergy; ss.
severe combined immunedeficiency; SCID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erythematosis, rheumatoid arthritis, autoimmune pulmonary inflammation,
Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Steininger RJ, Spaulding V;
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I, Agostino MJ,
Fechtel K;
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antithyroid; immune deficiency;
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99US-0119931.
99US-0120575.
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98US-0099229.
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Matches 15; Conservative
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Clark HF, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-205979/18.
P-PSDB; AAY94977.
                                                                                                                                                                                                                                                                                                                                                    WO200009552-A1
                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-1998
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Wong GG,
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ABV22746 standard; cDNA; 4215 BP.
                                                                                                             13-SEP-2002
                                                                                  ABV22746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. thrombocytopaenia), inflammatory allergic conditions (e.g. asthma), neurodegenerative disorders (e.g. haemophilia), and tumours. The polynucleotide sequences of the invention are also useful in gene therapy. ABM33610-ABM36232 represent the cDNA sequences of the invention that encode for novel human
                                                                                                                                                                                              Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; allergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial; tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                             .avallie ER, Collins-Racie LA, Evans C;
Agostino MJ, Bowman MR, Spaulding V, Wong GG;
Howes SH, Resnick RJ, Gulukota K, Graham JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3580;
                                                                                                                                                                         cDNA sequence #21 encoding novel human secreted protein
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100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0;
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                                                                                         ABK35630 standard; cDNA; 3580 BP.
                                                                                                                                                                                                                                                                                                                                                                29-MAR-2001; 2001WO-US10232.
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                                                                                                                                                (first entry)
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             2528 CCTTCTCCCCTGTT 2542
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Best Local Similarity 100.
Matches 15; Conservative
1 CCTTCTCCCCTGTT 15
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Clark HF, Fechtel K,
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                                                                                                                          Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;

(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid molecule (I) compa nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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100.0%; Score 15; DB 23;
100.0%; Pred. No. 4.5e+02;
0;
                                                              prostate expression marker cDNA 22737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 4005-4006; 11750pp; English.
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                                                                                                                                                           pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-MUN-2000; 2000US-211314P.
18-UUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
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(first entry)
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Matches 15; Conservative
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1053 CCTTCTCCCCCTGTT 1039

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CCTTCTCCCCCTGTT 15

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GenCore version 5.1.3

Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:29:32 ; Search time 47 Seconds

(without alignments)
97.876 Million cell updates/sec

Title: US-09-750-609-10

Perfect score: 15
Sequence: 1 ccttctcccctgtt 15
Sequence: 1 ccttctcccctgtt 15
Sequence: 441362 seqs, 153388381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Listing first 45 summaries

Listing first 45 summaries

Isved_Patents_Na:*

| /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
| /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
| /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
| /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 11, Appl Sequence 54, App Sequence 54, Appl Sequence 55, Appl Sequence 55, Appl Sequence 9, Appl Sequence 11, Appl Sequence 11, Appl Sequence 2, Appl Sequence 2, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appl Sequence 3, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 19, Appl Sequence 11, Appl Sequence 11, Appl Sequence 2, Appl Sequence 2, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 13, Appl Sequence 14, Appl Sequence Sequence 101, App Sequence 1, Appli Sequence 1, Appli Description US-09-502-653-11 US-09-605-785-747 US-08-975-316-55 US-08-975-316-55 US-08-975-316-55 US-08-381-43A-3 US-08-381-433A-3 US-08-381-433A-3 US-08-381-433A-3 US-08-379-496-1 US-08-379-496-1 US-08-379-496-1 US-08-379-496-1 US-08-379-496-1 US-08-379-496-1 US-08-379-496-1 US-08-379-496-1 US-08-955-729A-1 US-08-965-729A-1 US-08-306-691B-53 US-08-3108-306-691B-53 US-09-175-581-2 US-09-330-330-3 US-08-484-044-10 US-09-078-294-12 US-08-742-185-101 US-08-338-907-1 SUMMARIES DB Query Match Length 1074 1075 1075 1374 1514 1626 1875 2169 3182 3224 3279 3481 4287 4287 4396 4503 4503 6405 11613 11613 18073 43795 56516 Score Result 80  $\circ \circ \circ \circ \circ \circ$ O 00000 υ

Sequence 1, Appli Sequence 179, App Sequence 179, App Sequence 1, Appli Sequence 1, Appli Sequence 29, Appl Sequence 1, Appli Sequence 1, Appli Sequence 31, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli		own in SEQ ID Length 735; Indels 0; Gaps 0;	
US-09-218-207-1 US-09-38-907-179 US-09-218-207-179 US-09-108-216-3 US-09-103-84.0A-1 US-09-484-970B-82 US-08-619-542B-29 US-09-225-744A-1 US-09-225-744A-1 US-08-149-695-8 US-08-149-695-8 US-08-149-695-1 US-08-149-695-1 US-08-1377-228-1 US-08-1377-228-1 US-09-177-650-37 US-09-177-650-37 US-09-037-990B-48	ALIGNMENTS 1502653 celund tabbek ACTANASES 11 A 1999 00184 11 A 1999 00799 07 0/125,885 24 10/138,445 10	8721) inase sh DB 4; e+02;	9605785
4 89.3 56516 4 89.3 56520 4 89.3 441152 9 86.7 2431 4 86.7 2431 4 86.7 2431 4 86.7 2687 1 3 86.7 2687 1 4 82.7 2873 1 8 86.7 2873 1	RESULT 1 US-09-502-653-11/C Sequence 11, Application US/09502653 Patent No. 6331426 APPLICANT: By Invad, Mads Eskelund APPLICANT: By Invad, Mads Eskelund APPLICANT: Schlein, Martin APPLICANT: Schlein, Martin APPLICANT: Stergaard, Peter Rabbek APPLICANT: Stergaard, Peter Rabbek APPLICANT: Stergaard, Peter Rabbek APPLICANT: Stergaard, Peter Rabbek APPLICANT: Sholm, Carsten TITLE OF INVENTION: NOVEL GALACTANASES FILE REFERENCE: 5481.200-02-11 EARLIER APPLICATION NUMBER: US/09/502,653 CURRENT FILING DATE: 1999-02-11 EARLIER FILING DATE: 1999-06-07 EARLIER FILING DATE: 1999-06-07 EARLIER FILING DATE: 1999-06-07 EARLIER FILING DATE: 1999-06-10 EARLIER FILING DATE: 1999-06-10 EARLIER FILING DATE: 1999-06-10 NUMBER OF SEC ID NOS: 52 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 11	DNA  SM: Bacillus agaradhaerens ACI  SEX: CBS  CON: (1)(735)  INFORMATION: DNA encoding the INFORMATION: NO.12.  653-11  AS SECORE  14; Conservative 0; Miss  CCTTCTCCCCTGTT 15  CCTTCTCCCCTGTT 15  CCTTCTCCCCATGTT 291	5-747/c 47, Application US/0960578 6321716 FORMATION:
28 13. 29 13. 30 13. 31 13. 32 13. 33 13. 5 34 13. 5 40 11. 6 41 12. 7 44 12.	RESULT 1 US-09-502-653 Sequence 11 Sequence 11 Septent No. Septent	TYPE: DNA   CORCANISM: 1   FEATURE:   CORCANISM: 1   FEATURE:   COCTTON:   COTTON:   COCTTON:   C	RESULT 2 US-09-605-7457/C ; Sequence 747, Applic ; Patent No. 6321716 ; GENERAL INFORMATION:

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Gaps

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Length 1074;
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APPLICANT: and GRIERSON, Alastalir W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGHIN CONTENT
                                                                                                                                                                                                                                                                                                                                   Length 1074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT WESOLT TO SEQUENCE 54, Application US/09615192A

Sequence 54, Application US/09615192A

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Maderials and Methods for the
TITLE OF INVENTION: Maderials and Methods for the
TITLE OF INVENTION: Maderials and Methods for the
TITLE OF INVENTION: MAGNICATION OF 12
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT PILING DATE: 2000-07-12
PRIOR PELICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1996-09-11
PRIOR PELICATION NUMBER: US 08/713,000
PRIOR PELICATION NUMBER: US 09/169,789
PRIOR PELICATION NUMBER: US 09/169,789

PRIOR PELICATION NUMBER: US 09/169,789

SOFTWARE: FASTEEQ for Windows Version 3.0
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Pred. No. 2.8e+02;
0; Mismatches 1;
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Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                       REFERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 55, Application US/08975316; Patent No. 5952486; GENERAL INFORMATION:
                       37,007
                                                                                                                                                                                                                                                                                                                                 89.3%;
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                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 93.3
Matches 14; Conservative
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                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA; ORGANISM: Pinus radiata
US-09-615-192A-54
                                                                                                                                                                                                                                                                   linear
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Matches 14; Conserv
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US-08-975-316-54
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                                                                                                                            APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Oby, Craig H.
APPLICANT: Oby, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKSBERG Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GEIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.4; DB 4; Length 7 Pred. No. 2.7e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
                                                                   Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(738)
; OTHER INFORMATION: n=A,T,C or G
US-09-605-785-747
tu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 89.3%;
Best Local Similarity 93.3%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: WA
                                                                                       APPLICANT:
APPLICANT:
                                                                   APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
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Gaps

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Score 13.4; DB 4; Length 1374;
Pred. No. 2.8e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                               APPLICANT: LOUIS, Kathy A.
APPLICANT: LOUIS, Kathy A.
APPLICANT: Vale Jr., Mylie W.
APPLICANT: Donaldson, Cynthia J.
APPLICANT: Sawchenko, Paul
TITLE OF INVENTION: Cloning and Recombinant Production of
FILE REFERENCE: F41-90002
CURRENT APPLICATION NUMBER: US/08/482,746B
CURRENT APPLICATION NUMBER: US/08/482,746B
EARLIER APPLICATION NUMBER: US/08/1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lovenberg, Timothy W.
APPLICANT: Oltersdorf, Tilman
APPLICANT: Liaw, Chen
APPLICANT: Liaw, Chen
APPLICANT: Grigoriadis, Dimitri E.
APPLICANT: Grigoriadis, Errol B.
TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR
TITLE OF INVENTION: RECEPTORS
WINMER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: SEED and BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1993-111/

EARLIER PPLICATION NUMBER: US 08/353,537

EARLIER APPLICATION NUMBER: PCT/US94/05908

EARLIER PLING DATE: 1994-05-25

EARLIER PLING DATE: 1993-06-13

EARLIER FILING DATE: 1993-06-13

EARLIER FILING DATE: 1993-06-18

SEARLIER FILING DATE: 1993-06-18

NUMBER: OF SEQ ID NOS: 15

SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                    5-08-482-746-9
Sequence 9, Application US/08482746B
Patent No. 6399315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08381433A Patent No. 5786203 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.3%;
93.3%;
                                                                                                                                                                             APPLICANT: Perrin, Marilyn H. APPLICANT: Chen, Ruoping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DD 1080 CCTCCTCCCCTGTT 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (79)...(1371)
US-08-482-746-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
STATE: Washing
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STREET: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-08-381-433A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH:
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Pred. No. 2.8e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content FILE REFERENCE: 11000.100340 CURRENT APPLICATION NUMBER: 05/09/615,192A CURRENT FILING DATE: 200-07-12 PRIOR APPLICATION NUMBER: 05/09/615,192A PRIOR FILING DATE: 1997-11-21 PRIOR PLING DATE: 1997-11-21 PRIOR PLING DATE: 1997-11-21 PRIOR PLING DATE: 1996-10-09 PRIOR PLING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.4; DB 2;
Pred. No. 2.8e+02;
); Mismatches 1;
                                                                                                                           IBM Compatible
SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                   CURRENT APPLICATION DATE:
APPLICATION DATE:
APPLICATION NUMBER: US/08/975,316
FILING DATE:
CLASSIFICATION NUMBER: US/08/975,316
FILING DATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY AGENT INFORMATION:
NAME: SLEATH, Janet
RECISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000-0565
TELECOMMUNICATION 1000-0565
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 55
LENGTH: 1075
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; Sequence 55, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.; APPLICANT: Havukkala, 11kka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.3%;
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93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1075 base pairs
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      582 CCTTCTCCCCCTTTT 568
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CORGANISM: Pinus radiata
US-09-615-192A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 14; Conserve
                                                                                                                        COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
STATE: WA
                                                             98121
                                                                                                                                                                      SOFTWARE:
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US-08-975-316-55
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Sequence 1, Application US/08379496
Patent No. 5593833
GENERAL INFORMATION:
APPLICANT: MORRISON, Nigel A
APPLICANT: EISMAN, John A
APPLICANT: EISMAN, John A
APPLICANT: Assessment of Trans-Acting Factors Allelic
TITLE OF INVENTION: Assessment of Trans-Acting Factors Allelic
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      ö
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                                                                                                                                                                Length 1626;
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Sequence 21, Application US/09258373
GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Aiao, Sheng
TITLE OF INVENTION: HMGI(Y)-LAMA4* FUSION ONCOGENE,
TITLE OF INVENTION: HMGI(Y)-LAMA4* FUSION ONCOGENE,
CURRENT APPLICATION NUMBER: US/09/258,373
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 60/076,401
EARLIER FILING DATE: 1998-02-28
NUMBER OF SEO ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                              Score 13.4; DB 1;
Pred. No. 2.8e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13.4; DB 3;
Pred. No. 2.9e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Rothwell, Figg, Ernst & Kurz STREET: Suite 701-E, 555 13th Street.N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.24
CURRENY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 89.3%;
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                89.3%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 1755 CCTCCTCCCCTGTT 1769
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Best Local Similarity 93.33
Watches 14; Conservative
                                                                                                                                                                                                                                                                            Db 1157 CCTCCTCCCCCTGTT 1171
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                                                                                                                                                                                                                                               1 CCTTCTCCCCCTGTT 15
                 SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo Sapiens
US-09-258-373-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washingt
STATE: D.C.
COUNTRY: USA
                 STRANDEDNESS:
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                                       TOPOLOGY:
                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 21
LENGTH: 1875
                                                                                                                      US-08-381-433A-3
                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-09-258-373-21
                                                           FEATURE
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Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LOCKOLOGY, Tilman
APPLICANT: Oltersdorf, Tilman
APPLICANT: Liaw, Chen
APPLICANT: Liaw, Chen
APPLICANT: Liaw, Chen
APPLICANT: Grigoriadis, Dimitri E.
APPLICANT: DeSouza, Errol B.
TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2
TITLE OF INVENTION: RECEPTORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,433A
FLING DATE: 31-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: MCMSters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 690068.401C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: 723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 3:
                                                                          ATTORNEY AGENT INFORMATION:
NAME: MCMSters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 690068.401C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELER: 3723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 1:
SEGUENCE CHARATERISTICS:
LENGTH: 1514 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,433A
FILING DATE: 31-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08381433A Patent No. 5786203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.3%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1626 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 1045 CCTCCTCCCCTGTT 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 89.3
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCTTCTCCCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 44..1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-381-433A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-381-433A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
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Gaps

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NAME/KEY: misc_feature
OTHER INFORMATION: /note= "Nucleotides 2272 through 2729 are
OTHER INFORMATION: thrombin responsive element"; Human
                                                                                                                                                                                                                                                     Sequence 2, Application US/08965729A
Patent No. 6200751
GENERAL INFORMATION:
APPLICANT: Jian-Ming Gu and Charles T. Esmon
TITLE OF INVENTION: ENDOTHELIUM SPECIFIC EXPRESSION
TITLE OF INVENTION: REGULATED BY EPCR CONTROL ELEMENTS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
CITY: Atlanta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                Score 13.4; DB 1; Length 3182; Pred. No. 3e+02;
                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/965,729A FILING DATE: O7-NOV-1997 CLASSIFICATION:
                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,718
FILING DATE: 08-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
RESPERDENCE/POCKET NUMBER: OMRF 164 PCT
TELECOMMUNICATION INFORMATION:
TELEPAX: 404-873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9303077 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 3224 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                89.3%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 2759 CCTTCTCCCCCTTT 2773
                                                   Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                        414 CCTTCTCCCTTGTT 428
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 30309-4530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GA
                                                                                                                                                                                                                                      US-08-965-729A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US93-03077-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-965-729A-2
                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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APPLICANT: Fu, Ying-Hui
APPLICANT: Fu, Ying-Hui
APPLICANT: Friedman, David L.
APPLICANT: Pizzuti, Antonio
APPLICANT: Penwick, Raymond G.
TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbriaht for
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                         Length 2169;
                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,044
                                                                                                                                                                                                                                                                                                                                                         Score 13.4; DB 1;
Pred. No. 2.9e+02;
0; Mismatches 1;
FILING DATE: 02-WAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ENST, BATDARG G
REGISTRATION NUMBER: 30,377
REPERBENCE/DOCKET NUMBER: 1871-114
TELECHMUNICATION INFORMATION:
TELEPHONE: 202 783-6040
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2169 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/019,940
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5443
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08484044 Patent No. 5552282
                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-08-484-044-11
                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                       cuery Match 89.3%;
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 CCTTCTCTCCTGTT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCTTCTCCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Houston
STATE: Terr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 713/
                                                                                                                                                                                                                                                                               TOPOLOGY:
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US-08-484-044-11
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Gaps

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NAME/KEY: misc_feature
OTHER INFORMATION: /note= "Nucleotides 3130 through 3350 are an
OTHER INFORMATION: endothelial specific element"; murine
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OTHER INFORMATION: /note= "Nucleotides 3007 through 3014 are a
OTHER INFORMATION: thrombin responsive element"; murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
OTHER INFORMATION: /note= "Nucleotides 2270 through 2840 are a
OTHER INFORMATION: large endothelial specific element"; murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
OTHER INFORMATION: /note= "Nucleotides 2990 through 3061 are a
OTHER INFORMATION: serum response element"; murine
APPLICATION NUMBER: US/08/965,729A
CLASSIFICATION
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 66/030,718
FILING DATE: 08-NOV-1997
ATTORNEY AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET UNPERRY OMFF 164 PCT
TELEPONMUNICATION INFORMATION:
TELEPHONE: 404-873-8794
TELEFAX: 404-873-8795
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3481 base pairs
TYPE: nucleic acid
STRANDEDRESS: single
TOPPLOGY: linear
MOLECULE TYPE: DNA (Genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: December 11, 2002, 15:30:47
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93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 89.3
Best Local Similarity 93.3
Matches 14; Conservative
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Patent No. 6200751

GENERAL INFORMATION:
APPLICANT: Jian-Ming Gu and Charles T. Esmon
TITLE OF INVENTION: REGULATED BY EPCR CONTROL ELEMENTS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Pred. No. 3e+02;
0; Mismatches 1; Indels 0
    APPLICANT: Board of Regents, The Universityof Texas System APPLICANT: Gaynor, Richard B. APPLICANT: Wu, FOON Kin TITLE OF INVENTION: REGULATING GENE EXPRESSION TITLE OF INVENTION: REGULATING GENE EXPRESSION
                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03077
FILING DATE: 19930331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UTFD270PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/862,025
FILING DATE: April 2, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                        ADDRESSEE: Arnold White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kammerer, Patricia A. REGISTRATION NUMBER: 29,775 REFRENCE/DOCKET NUMBER: UTFD TELECOMMUNICATION INFORMATION: TELEPHONE: 713-787-1540 TELEFAX: 713-749-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.3%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 3279 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCTTCTCCCCCTGTT 15
                                                                                                                            NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US93-03077-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-965-729A-1
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Gaps

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Score 13.4; DB 4; Length 3481; Pred. No. 3e+02; 0; Mismatches 1; Indels 0;

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GenCore version 5.1.3

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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 14:35:52; Search time 52.5 Seconds

(without alignments)

111.409 Million cell updates/sec

15 Sequence: US-09-750-609-10

Sequence: 1 ccttctcccctgtt 15

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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Published_Applications_NA:*

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4: /cgn2_6/ptodatta/2/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodatta/2/pubpna/USO7_NEW_PUB.seq:*
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13: /cgn2_6/ptodatta/2/pubpna/USO9_PUBCOMB.seq:*
14: /cgn2_6/ptodatta/2/pubpna/USO9_PUBCOMB.seq:*
14: /cgn2_6/ptodatta/2/pubpna/USO0_PUBCOMB.seq:*
14: /cgn2_6/ptodatta/2/pubpna/USO0_PUBCOMB.seq:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 1704, Ap	Sequence 1577, Ap	Sequence 3234, Ap	Sequence 84, Appl	Sequence 1570, Ap	Sequence 13104, A	Sequence 1692, Ap	Sequence 3063, Ap	Sequence 3349, Ap	Sequence 4063, Ap	Sequence 10753, A	Sequence 96, Appl	Sequence 10470, A	Seguence 1267, Ap	Sequence 1268, Ap	Sequence 1269, Ap	Sequence 1267, Ap	Sequence 1268, Ap	Sequence 1269, Ap
ΩI	US-09-764-864-1704	US-09-954-456-1577	US-09-880-107-3234	US-10-001-835-84	US-09-833-381-1570	US-09-864-761-13104	US-09-764-864-1692	US-09-764-877-3063	US-09-764-877-3349	US-09-974-300-4063	US-09-783-590-10753	US-09-712-363-96	US-09-783-590-10470	US-09-946-807-1267	US-09-946-807-1268	US-09-946-807-1269	US-09-795-668-1267	US-09-795-668-1268	US-09-795-668-1269
DB	10	10	10	σ	10	10	10	10	10	10	10	6	10	0	σ	σ	10	10	10
% Query Match Length DB	15857	389	389	482	493	594	8894	8894	16877	198	264	315	363	. 401	401	401	401	401	401
% Query Match	100.0	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	89.3	89.3	89.3	89.3	89.3	89.3	89.3	89.3	89.3	89.3
Score	15	14	14	14	14	14	14	14	14	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4
Result No.		0	c 3	O 4	0	9	c 7	8	გ ე	10	11	c 12	c 13	14	15	16	17	18	19

Sequence 1267, Ap Sequence 1268, Ap Sequence 1269, Ap Sequence 332, App Sequence 555, App Sequence 210, App Sequence 1100, Ap Sequence 114, App Sequence 51, App Sequence 717, App Sequence 747, App Sequence 748, App Sequence 138, App Sequence 138, App Sequence 138, App Sequence 138, App Sequence 11, Appli Sequence 1,	Sequence 3, Appli Sequence 401, App Sequence 189, App	Sequence 123, APP Sequence 703, App Sequence 298, App
US-09-795-686-1267 US-09-795-686-1268 US-09-954-531-32 US-09-954-531-355 US-09-962-832-210 US-09-962-832-210 US-09-962-832-210 US-09-964-456-1100 US-09-964-456-1100 US-09-964-456-1100 US-09-964-456-1100 US-09-964-761-314 US-09-967-768A-134 US-09-977-68A-134 US-09-977-848-134 US-09-798-445-393 US-09-925-301-438 US-09-925-301-438 US-09-925-301-438 US-09-925-301-438	US-09-881-401-3 US-09-822-830A-401 US-09-974-298-189	US-09-842A-703 US-09-864-864-298
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## ALIGNMENTS

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APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
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       Sequence 1704, Application US/09764864

Patent No. US2002013275341

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper;

NUMBER OF SEQ ID NOS: 1792

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-954-456-1577/c
US-09-764-864-1704
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PATEUT NO. 022020100307A1

GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and
FILE REFERENCE: DEX-0277
CURRENT APPLICATION NUMBER: US/10/001,835
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,997
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: Patentin Version 3.1
SEQ ID NO 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-83-381-1570/c
US-09-83-381-1570/c
Sequence 1570, Application US/09833381
Sequence 1570, Application US/09833381
Sequence 1570, Application US/09833381
Sequence 1570, Application US-09-83-81
GENERAL INFORMATION: Neith E.
TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1570
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100.0%; Pred. No. 2.2e+02;
iive 0; Mismatches 0;
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US-09-864-761-13104
; Sequence 13104, Application US/09864761
                                                                                                                   Sequence 84, Application US/10001835 Patent No. US20020160387A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | LOCATION: (1)...(493)
| OTHER INFORMATION: n - A,T,C or G
US-09-833-381-1570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0%; P Matches 14; Conservative 0;
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Best Local Similarity 93.3
Matches 14; Conservative
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296 CCTTCTCCCCTGT 283
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ORGANISM: Homo sapien
                                                                            RESULT 4
US-10-001-835-84/c
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Sequence 3234, Application US/09880107

Patent No. US/0020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: Scherf, Uwe

APPLICANT: Gene Expression Profiles in Liver Cancer:

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer:

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR PRILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3234
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                  PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR PILING DATE: 2000-09-25
PRIOR PELLOR DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SEQ ID NO 1577
LENGTH: 389
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CCATION: (1).(389)

CTHER INFORMATION: n = a or c or g or t

US-09-880-107-3234
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; OTHER INFORMATION: n=a,t,g or c
US-09-954-456-1577
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Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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ORGANISM: Homo sapiens
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Patent No. US20020147140A1

GENERAL INFORMATION:

APPLICATION:

TILE REFERENCE: PC005

CURRENT APPLICATION NUMBER: US/09/764.877

CURRENT APPLICATION NUMBER: US/09/764.877

CURRENT APPLICATION ADDITION: US/09/764.877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3063

LENGTH: 8894
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CURRENT FILING DATE: 2001-01-17
(Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3.057
LENGTH: 16877
                                                                    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT223
FILE REFERENCE: PT223
FULL REFERENCE: PT223
FULL REFERENCE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1692
LENGTH: 8894
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; I
2.7e+02;
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100.0%; Pred. No. 2...
0; Mismatches
Sequence 1692, Application US/09764864 Patent No. US20020132753A1 GENERAL INFORMATION:
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; Patent No. US20020147140A1
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100.08; Pie
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Best Local Similarity 100.
Matches 14; Conservative
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-864-1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-09-764-877-3063
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; ORGANISM: Homo sapiens
US-09-764-877-3349
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                                                                                                                         APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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100.0%; Pred. No. 2.2e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: MAP TO AL136968.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.5

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.68

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7

US-09-864-761-13104
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13104
EBNGTH: 594
                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-08-03
PRIOR PLILICATION NUMBER: GB 24263.6
PRIOR FILING-DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00665
FILLING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                               APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 93.3
Best Local Similarity 100.
Matches 14; Conservative
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Patent No. US20020048763A1
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RESULT 7 US-09-764-864-1692/c

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APPLICANT: Rotatein, Savid H.
APPLICANT: Rotatein, Savid H.
APPLICANT: Rotatein, Savid H.
APPLICANT: Rotatein, Savid H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-03201
CURRENT APPLICATION NUMBER: 05/09/712,363
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR APPLICATION NUMBER: 60/119,531
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-14
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
SPRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARRE: FastSEQ for Windows Version 4.0
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Patent No. US20020110850A1
GENERAL INFORMATION.
APPLICANT: Districk J.
APPLICANT: Li, Hadodong
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Roben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REPERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
                                                 Length 264;
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                                                                                                     Indels
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                                                   DB 10;
                                                 Score 13.4; DB Pred. No. 4e+02; Mismatches
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US-09-712-363-96
                                                                                                                                                                                                                                                                                                     US-09-712-363-96/c
; Sequence 96, Application US/09712363
; Patent No. US20020164588A1
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93.3%;
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                                                   Query Match 89.3
Best Local Similarity 93.3
Matches 14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
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  US-09-783-590-10753
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Sequence 10753 Application US/09783590

Sequence 10753 Application US/09783590

SEQUENCE OF US/00110850AI

APPLICANT: Haseltine, William A.

APPLICANT: Li, Haodong

APPLICANT: Li, Haodong

TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2

FILE REPERBUCE: PO-16.2C1

CURRENT FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: US/09/783,590

CURRENT FILING DATE: 1995-04-12.

PRIOR FILING DATE: 1995-04-12.

PRIOR FILING DATE: 1995-04-12.
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     Length 16877;
                                                                                                                                                                                                                                                                      ; Sequence 4063, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka. Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2000-10-06
; PRIOR FILING DATE: 2000-10-06
; PRIOR FILING DATE: 2000-10-06
; PRIOR FILING SATE: 2000-10-06
93.3%; Score 14; DB 10; I
100.0%; Pred. No. 2.9e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Bacillus licheniformis US-09-974-300-4063
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93.3%;
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 93.3
Matches 14; Conservative
  Query Match 93.3
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                 1269 CCTTCTCCCCCTGT 1256
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US-09-974-300-4063
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LENGTH: 264
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LENGTH: 198
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Score 13.4; DB 9; Length 401;
Pred. No. 4.2e+02;
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Pred. No. 4.2e+02;
0; Mismatches 1;
                                                              APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-8
NUMBER OF SED ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
TEACH TO THE TO 
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CURRENY APPLICATION NUMBER: US/09/946,807
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1268
LENGTH: 401
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Patent No. US20020165144A1
GENERAL INFORMATION:
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93.3%;
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Best Local Similarity 93.3
Matches 14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
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         Patent No. US20020165144A1 GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-946-807-1267
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CORGANISM: Homo sapiens
US-09-946-807-1268
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Pred. No. 4.1e+02;
0; Mismatches 1;
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LOCATION: (112)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (123)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (145)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (145)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (193)
OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (105)
OTHER INFORMATION: n equals a,t,g, or
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin 363
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (226)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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LOCATION: (352)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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Best Local Similarity 93.3%;
Matches 14; Conservative
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LOCATION: (336)
                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature LOCATION: (47)
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                                                                                                                                                                                                                                                                   TYPE: DNA
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US-09-946-807-1267; Sequence 1267, Application US/09946807

RESULT 14

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Length 401;

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December 11, 2002, 13:27:12 ; Search time 1661 Seconds (without alignments) 146.257 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                        16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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15
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                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                        Sequence:
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                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		AZ284882 RPCI-23-4	AV335397 AV335397	AL708655 DKFZp686J	AV067076 AV067076	F07213 HSC1ZB021 n	. T08889 EST06781 In
	ID	:		AV335397	AL708655	AV067076	F07213	T08889
	DB		17	10	6	6	14	14
	Query Match Length DB ID		181	226	246	297	378	393
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Tel: 301 838 0200 Fax: 301 838 0208
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FEATURES

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246 bp mRNA linear EST 22-MAR-2002
DKF2p686J0853_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKF2p686J0853 5', mRNA sequence.
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oblongata"
         polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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                                                                                                                                                                                                                                      system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                   ,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation % \left( 1\right) =\left\{ 1\right\} =\left\{ 1
                                                                                                                                                                                                                                                                                                                                                                               19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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This is the 5' sequence of the clone insert
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The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-9226
Fax: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI: Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DHIOB electrocompetent cells (BRL Life Technologies).
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BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 442 row: E column: 20 Seg primer: T7
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Mr.http://genome-gsc.riken.go.jp,
Sasaki,N., Izawa.M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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100.0%; Pred. No. 5.5e+03;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="c57BL/6J"
/db.xref="taxon.10090"
/clone="rpCI-23-442E20"
/clone=lib="RPCI-23"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
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AV335397
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SOURCE

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/Lissue_type="small intestine"
//Lissue_type="small intestine"
//dev_stage="adult"
//d
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HSC12B021 normalized infant brain cDNA Homo sapiens cDNA clone
c-15b02, mRNA sequence.
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/clone="c-12b02"
/sex="Female"
/tissue_type="total brain"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=rotal brain;
total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
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1 (bases 1 to 378)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
/clone="2010200P09"
/clone_lib-"Mus musculus small intestine C57BL/6J adult"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Genexpress_library_idt: C: Genexpress_sequence_idt: ylc-lzb02
Seq primer: (-21)M13_universal.
Location/Qualifiers
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Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 3316947280
Fax: 33160778698
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C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
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/db_xref="taxon:9606"
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F07213.1 GI:672862
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Best Local Similarity 100.
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Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 297)
                                                                                                                                                                                                                                                                                                                1. .246

/organism="Homo sapiens"

/db_xref="haxon:9606"

/clone="bkFzp686J0853"

/clone="lib="686 (synonym: hlcc3)"

/tissue_type="human skeletal muscle"

/dev_stage="adult"

/dev_stage="adult"

/lab_host="hHn08"

/note="vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB; cDNA-collection"
   Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

No s1 sequence available.
                                                                                                                                                                           This clone (DKPZp686J0853) is available at the RZPD in Berlin. Please contact the RZPP: Ressourcentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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                                                                                                                                                                                                                          1993 1993 299 mRNA linear EST 03-AUG-1993 EST06781 Infant Brain, Bento Soares Homo sapiens CDNA clone HIBBL71 5' end similar to p87 transporter-like protein, mRNA sequence. 1708899 GI:389917
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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lafmid BA vector. Clone library from B.Soares,
Dept. Columbia University, USA. Normalization_m
Bento Soares, P.N.A.S in press" 2 others
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100.0%; Pred. No. 6.4e+03;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .393
/organism="Homo sapiens"
/db_xref="ATCC (inhost):85383"
/db_xref="taxon:9606"
/clone="HIBBL71"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 3018699423
Email: mdadams@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers
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Best Local Similarity 100.
Matches 15; Conservative
                                                                             Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                 193 CCTTCTCCCCTGTT 207
                                                                                                                                    1 CCTTCTCCCCCTGTT 15
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KEYWORDS
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KEYWORDS
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T08889
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TABE07P 401 bp DNA linear GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 8e07, forward sequence, genomic
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Rockville, MD. Genomic DNA isolated from a cloned population of
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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1 (bases 1 to 401)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Hall, N., Bowman, S., Lennard, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CBl0 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                           phasianinae; Gallus.

1 (bases 1 to 399)
Bucrstedde.J.M.
Gallus gallus bursal lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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100.0%; Score 15; DB 9; is Best Local Similarity 100.0%; Pred. No. 6.4e+03; Matches 15; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
/8 c 103 g 97 t
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                                                                                                                                                                                                                                                                                                                                                     1. .399
//organism="callus gallus"
/db_xref="taxon:9031"
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/clone_lib="riken1"
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/clone="8e07"
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Homo sapiens
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Seq primer: T3 ET from Amersham
High quality sequence stop: 396.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pare, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                    BI706542 403 bp mRNA linear EST 13-FEB-2002 fq07c03.yl Zebrafish adult retina cDNA Danio rerio cDNA clone 4790765 5' similar to TR:Q9UH03 Q9UH03 BK250D10.3;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
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Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fal: 314 286 1810
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   100.0%; Score 15; DB 17;
illarity 100.0%; Pred. No. 6.4e+03;
Conservative 0; Mismatches
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    .403
    /organism="Danio rerio"

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/clone="4790765"
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Best Local Similarity 100.

Matches 15, Conservative
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                                                       Best_Local Similarity
Matches 15; Conserv
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AW139708/c
LOCUS
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/Glone="Image:271800"
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//Jab_bost="Nucl_CGAP_Sub3"
//Jab_bost="Nucl_CGAP_Sub3"
//Jab_bost="Nucl_CGAP_Sub3"
//Jab_bost="Nucl_CGAP_Sub3"
//Jab_bost="Nucl_CGAP_Sub3"
//Jab_bost="Nucl_CGAP_Largered library derived from NCI_CGAP_Sub1 library is a subtracted library derived from BI. BI constitutes a mixture of 21
normalized or subtracted NCI_CGAP_Largered library
derived from BI. BI constitutes a mixture of 21
normalized or subtracted NCI_CGAP_Largered library
derived from BI. BI constitutes a mixture of 21
normalized or subtracted NCI_CGAP_Largered library
derived from BI. BI constitutes a mixture of 21
nCI_CGAP_Raid. NCI_CGAP_Largered NCI_CGAP_Largered library
NCI_CGAP_Raid. NCI_CGAP_Largered NCI_CGAP_Largered library
NCI_CGAP_Enr23, NCI_CGAP_Lub5, NCI_CGAP_Lub4,
NCI_CGAP_Enr23, NCI_CGAP_Lub5, NCI_CGAP_Lub4,
NCI_CGAP_Enr25, NCI_CGAP_Lub5, NCI_CGAP_Lub4,
NCI_CGAP_Enr26, NCI_CGAP_Lub5, NCI_CGAP_Lub4,
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NCI_CGAP_Enr28, NCI_CGAP_Lub6, NCI_CGAP_Lub6,
NCI_CGAP_Enr28, NCI_CGAP_Lub6, NCI_CGAP_Lub6,
NCI_CGAP_Enr28, NCI_CGAP_Lub6, NCI_CGAP_Lub6,
NCI_CGAP_Enr28, NCI_CGAP_Lub6, NCI_CGAP_Lub6,
NCI_CGAP_Raid pool 1 LLAM 3334-3337, 3682-3683,
3722-3725, 3776-3778 (IMAGE CloneIDS 1237096-1235831,
1471388-1472903, 1492104-1493255); NCI_CGAP_Lub6 pool 1
LLAM 3572-3372, 3373-3385 (IMAGE CloneIDS 1257096-1258631,
1469064-1470983, 1475592-1476743); NCI_CGAP_PR22 pool 1
LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS
9885068 (1MAGE CloneIDS
9885068 (1MAGE CloneIDS
988508                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G. E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 151-216, >(GGGA)
)#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI_CGAP_CO10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145531). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 410)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
UI-H-BII-aeb-a-03-0-UI.sl NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2718605 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6, 791-806.
TAG_LIB=NCI_CGAP_Kid3
TAG_TISSUB=kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                 AW139708.1 GI:6144426
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100.0%;
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Unpublished (1997)
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9

VERSION

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/organism=""Homo" saplens"
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/lab_bost="nbH10B (Life Technologies)"
/nab_bost="nbH10B (Life Technologies)
/nab_subtracted library derlyed from NCI_CGAP_Sub6. The
single-stranded DNA preparation of NCI_CGAP_Sub6 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI_CGAP_Kid3 pool 1 LLAM
3343-3377, 3682-3683, 3798-3803 (IMAGE ClonelDS
1322376-1323911, 1456008-1456775,1500552-1502855);
/nCI_CGAP_CGCA pool 1 LLAM 3184-3167, 3716-3778
/nCI_CGAP_CGCA pool 1 LLAM 3184-3167, 3716-3778
/nCI_CGAP_CGCA pool 1 LLAM 3184-3167, 3716-3778
/nCI_CGAP_CGCA pool 1 LLAM 3164-3167, 3716-3720,
/nCI_CGAP_CGCA pool 1 LLAM 3168-1472991, 1520904-152439,
/nCI_CGAP_CGCA pool 1 LLAM 3168-1298631, 1469064-1470983,
/nCI_CGAP_CGCA pool 1 LLAM 3168-12061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 7169061, 716
                                                                                                         Contact: Robert Strausberg, Ph.D.

Email: cgapbs remail.nih.gov

The sequence contained an oligo-dr track that was present in the oligonoutleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the WWW-bio.linl.gov/bbrp/image/image.html
                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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100.0%; Pred. No. 6.5e+03;
:1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_LIB=NCI_CGAP_Brn50
TAG_TISSUE=brain
TAG_SEQ=TTTCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research 6, 791-806.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Matches 15; Conservative
                                                                                Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 CCTTCTCCCCTGTT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                POLYA-Yes
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ORIGIN
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BG961625/c
REFERENCE
                            AUTHORS
                                                                                                         JOURNAL
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                                                   TITLE
                                                                                                                                         COMMENT
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BF514910 I GI:11600078
                                                                                                                                                                                                                                          4.20 DP mRNA linear EST 02-MAR-2000 UI-HF-BNO-alk-h-12-0-UI.rl NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079943 5', mRNA sequence.
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Starayotas Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"vector: pT7T3-Pac; Site_1: NoLI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (3.5-4,4kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Scares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/bbrp/image/image.html

Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 420)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 15; DB 10; 100.0%; Pred. No. 6.5e+03;
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        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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              Conservative
                                                                                           396 CCTTCTCCCCTGTT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCTTCTCCCCCTGTT 15
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                                                              1 CCTTCTCCCCCTGTT 15
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nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
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                                                                                                                                                                                                                                                                                     DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                 AW504644/C
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KEYWORDS
              Matches
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SOURCE
                                                                                                                                                                                                        RESULT 11
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QV2-NN0045-211100-494-c07 NN0045 Homo sapiens cDNA, mRNA sequence.
BQ339760.1 GI:20999826
BST
                  1 (bases 1 to 430)
Hertzberg, M., Aspeborg, H., Erlandsson, R., Bjorkbacka, H., Hiltonen, T., Karlsson, J., Teerl, T., Gustafsson, P., Bahlerao, R., Jansson, S., Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M., Sandberg, G. and Gene expression in Populus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-21100-494-c07&t3=2000-11-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 29.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 431)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:3694"
/clone_lib="Populus flower cDNA library"
/note="Organ: flower"
                                                                                                                                                                                                                   Department of Biotechnology
Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
Tel: 46 8 790 8287
Fax: 46 8 245452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 15; DB 13;
llarity 100.0%; Pred. No. 6.5e+03;
Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                 Email: rikerl@biochem.kth.se.
Location/Qualifiers
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                                                                                                                                                                       Unpublished (2001)
Contact: Erlandsson R
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Fax: +55-11-2707001
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/db_xref="taxon:9606"
/dbo=lib="cr0642"
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/dev_stage="Adult"
/note="Organ: colon; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from OMESTES PCR (U.S. Letters Patent application No. 196 / 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carralho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                  EST 12-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-CT0642-240401-007-c09&t2=2001-04-24&t4=1)
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High quality sequence stop: 376.
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Populus balsamifera subsp. trichocarpa
Populus balsamifera subsp. trichocarpa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
ысуюць25
PMO-CTO642-240401-007-C09 CT0642 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                   BG961625.1 GI:14379796
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AX194634 Sequence X91127 Homo sapien BC000563 Homo sapi M65105 Human norad

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HUMNORTR

HSNETEX9 BC000563

AX194629

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AX194629 Sequence

SUMMARIES

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                     Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Listing first 1000 summaries
                                                                        OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  AUTHORS Chu.T., Blumenfeld,M. and Cohen,D.  TITLE Biallelic markers derived from genomic regions carrying genes involved in central nervous system disorders  JOURNAL Patent: WO 0151659-A 99 19-JUL-2001;  FEATURES  Source  Joganism-"Homo sapiens"  Ab xref="taxon:9606"  Primer_bind 20. 39  misc_feature 76. 94  misc_feature 76. 94  misc_feature 76. 94  misc_feature 95  Note="16-2-76 misl"  misc_feature 700-e":16-2-76 potential probe"  yariation 700-e":16-2-76 potential probe"  Anote="16-2-76 misl"  Misc_feature 700-e":16-2-76 misl"  primer_bind 700-e":16-2-76 misl"  Mote="16-2-76 misl"  Anote="16-2-76 misl"  Anote="1	tch al Similari 15; Cons CCTTCTCGCCC CTTCTCGCCC AX194634 AX194634 AX194634 AX194634 AX194634 AX194634	sapi yota lia; lia; ases b elic ved t: W	misc_feature 194218  variation 700te="16-2-187 potential probe"  variation 700te="16-2-187 is polymorphic base A or G"  misc_feature 207225  primer_bind 240265  primer_bind 240260 225 g 227 t 4 others  ORIGIN 100.0%; Score 15; DB 6; Length 920;
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Homo sapiens partial SLC6A2 gene for norepinephrine transporter,
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Porzgen, P., Bonisch, H., Hammermann, R. and Bruss, M.
The human noradrenaline transporter gene contains multiple
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Porzgen, P., Bonisch, H. and Bruss, M.
Molecular cloning and organization of the coding region of the man norrepinephrine transporter gene
Biochem. Biophys. Res. Commun. 215 (3), 1145-1150 (1995)
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Web site: http://www.insc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 5 Row: i Column: 7
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TFSTFLLALFCITKGGIYVLTLLDTFRAGTSILFAVLMEAIGVSWFYGVDRFSNDIOO
MMGFRDGLYWRLCWKFVSPAFLLFVVVVSIINFKPLTYDDYIPPPWANWVGWGIALSS
MWGLYRIYVIYKFLSTGSLWFALAYGTIPENEHHLVAQRDIRQFQLQHWLAI"
378 c 373 t
                 PRI 12-JUL-2001
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KFDNNCYRDALLTSSINCITSFVSGFAIFSILGYMAHEHKVNIEDVATEGAGLVFILY
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                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency
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/protein_id="AAH00563.1"
/db_xref="G1:12653577"
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אות בפרטטטסט 1411 bp mRNA linear Pi
Homo sapiens, clone IMAGE:3162672, mRNA, partial cds.
BC000563
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/db_xref="taxon:9606"
/clone="InAGE:3162672"
/tissue_type="Brain, neuroblastoma"
/clone_lib="NIH_MGC_19"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Mammalia; Eutheria; 1
1 (bases 1 to 1411)
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Matches 15; Conservative
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VERSION KEYWORDS SOURCE

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HUMCULXVA1 5161 bp mRNA linear PRI 31-DEC-1994
Homo sapiens alpha-1 type XV collagen mRNA, complete cds.
L25286
                                                                                   Identification of a previously unknown human collagen chain, alpha 1(XV), characterized by extensive interruptions in the triple-helical region Psecon Natl. Acad. Sci. U.S.A. 89 (21), 10144-10148 (1992) 93066196
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Myers, J.C., Kivirikko, S., Gordon, M.K., Dion, A.S. and Pihlajaniemi, T.
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Kivirikko,S., Heinamaki,P., Rehn,M., Honkanen,N., Myers,J.C. and
Pihlajaniemi,T.
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alpha-1 type XV collagen.
momo sapiens (tissue library: Clontech bases 955-5167) umbilical
cord (bases 1-954) cDNA to mRNA.
HOMO sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
//db_xref="taxon:9606"
/tissue_type="placenta"
/tissue_type="glil from Clonetech Laboratories"
583 c 644 g 392 t
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/tlssue_type="umbilical cord (bases 1-954)"
/tlssue_lib="Clontech bases 955-5167"
                           1 (bases 1 to 2127)
Myers,J.C., Kivirikko,S., Gordon,M.K., Dion,A.S. and
Pihlajaniemi,T.
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1. .5161
/organism="Homo sapiens"
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/note="putative"
/citation=[2]
/label=5'UTR
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/gene="COL15A1"
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1 (bases 1 to 1983)
Pacholczyk,T., Blakely,R.D. and Amara,S.G.
Expression oloning of a cocaine- and antidepressant-sensitive human noradrenaline transporter.
Nature 350 (6316), 350-354 (1991)
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/protein_id="AAA59943.1"
/do_xref="do1:189258"
/db_xref="do1:189258"
/db_
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1. .1983
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Human, cDNA to mRNA.
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/gene="NAT1"
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AC020425 14621 bp DNA linear HTG 03-JAN-2000 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 61956)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was identified as CDM:10213135 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.

* Coation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea; Drosophilidae; Drosophila.

[ base 1 to 14621)
Adams, M. and Venter, J.C.
Direct Submission
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Unpublished
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/db_xref="taxon:2227"
2792 c 2769 a 4724 +
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44;
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AC020425.1 GI:6664472
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INTPPTPSSPREDMELSGEPVPEGTLETTNMSI I OHSSPKQSSGEILAUTLEGVHSVD
OPDITDSGSGAGAFLDIAERNILAATAAGLAEVPISTAGEAEASSVPTGGPTLSMSTE
NPEGVYPTGPDNEERTAATAGEAELASMPGEVVASORVAFGELDLSMSAQSLGEEAT
VGPSSEDSLTTAAAATEEDELSASGVPTDGLAPITAAPAFRAYTSGPODEED
LAAATTEEPLITAGGEESGSPPPDGPPLPTVAPERNITPAQREHVGMKGQAGPKGE
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PSPCLUGIPGOKRQTDVFMGPPGSPAEDGPGEBEGPGPBGGPGVUGAFGLPGWKGEKG
ARAPNGSVGEKGDPGVNGLPGPPGKKGQAGPPGVWGPPGPPGPPGPPGCTWGLGFE
DTEGSGSTQLLNEPKLSRPTAAIGLKGEKGDRGPKGERGMDGASIVGPPGPRGPPGII
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TIVRKAERYSLPIVNLKGQVLFNNMDSIFSGHGGQFNMHIPIYSFDGRDIMTDPSWPQ
KVIWHGSSPHGVRLVDNYCEAWRTADTAVTGLASPLSTGKILDQKAYSCANRLIVLCI
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EQGEKGEPGAILTEDIPLERLMGKKGEPGMHGAPGPMGPRGPPGHKGEFGLPGRPGRP
GLNGLKGTKGDPGVIMQGPPGLPGPPGPPGPPGAVINIKGAIFPIPVRPHCKMPVDTA
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GDKGFKGEKGEKGBINGSFLMSGPPGLPGNPGPAGQKGETVVGPQGPPGAPGLPGPPG
                                                                                                                                                                                                                                                                             /translation="MAPRRNNGQCWCLLMLLSVSTPLPAVTQTRGATETASQGHLDLT
QLIGDPLPSSVSFVTGYGGFPAYSFGPGANVGRPARTLIPSTFFRDFAIRLVVKPSST
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                                                                                                                                                        /label=CDS
/product="alpha-1 type XV collagen"
/protein_id="AAA58429.1"
/db_xref="G1:461397"
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/note="putative"
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4254. .5161
/gene="COL15A1"
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4631. .4636
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5126. .5131
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/citation=[2]
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/gene="COL15A1"
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TITLE JOURNAL COMMENT

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73 33072: contrig of 766 bp in length

73 33838: contig of 766 bp in length

73 33838: contig of 766 bp in length

73 34239: contig of 682 bp in length

73 3420: contig of 682 bp in length

73 3420: contig of 747 bp in length

74 3567: contig of 655 bp in length

75 3622: contig of 655 bp in length

75 36322: qap of 100 bp

75 36322: qap of 100 bp

75 36322: qap of 100 bp

75 36398: contig of 675 bp in length

75 36398: contig of 672 bp in length

75 36398: contig of 672 bp in length
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contig of 677 bp in
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13. contig of 761 bp 1

gap of 100 bp

74. contig of 761 bp 1

gap of 100 bp

12. contig of 668 bp in
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of 689 bp
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of 749 bp
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35: contig of 683 bp
gap of 100 bp
                                       100 bp
645 bp
100 bp
674 bp
100 bp
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15570: contig of 675 bp
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contig of 660 bp
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13254: contig of
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contig of
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28117: contig
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38547: con
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14795: con'
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Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, M., Hagos, B., Heaford, A., Horton, L., Hulme, M., Illiev, I., Johnson, R., Jones, C., Kamat, A., Katlas, A., Kalls, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Macchan, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Merquis, N., Mathews, C., Macdonald, P., Major, J., Merphy, T., Naylor, J., Nguyen, C., Norman, C., M., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Feback, M., Riley, R., Schauer, S., Schupback, R., Seman, S., Severti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramaina, A., Talamas, J., Tesfaye, S., Theodore, J., Volan, Wilson, Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Ville, M., Wilson, J., Zambek, L., Zimmer, A. and Zody, M., Zantor, Contern Contern Contern Contern Contern Contern Contern Contern Contern Conternation, S., Submission, M., Whyman, D., Ye, W.J., Young, G., Marchan, C., Shands, J., Man, C., Shands, J., Nord, M., Wille, R., Zimmer, A. and Zody, M., Santos, J., Warel, R., Submission, M., Whyman, M., Weller, M., Shands, J., Shands, J., Submission, M., Whyman, M., Santos, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: project Information
Center project name: L16579
Center clone name: 117_1_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p of 100 bp 100 conting of 671 bp in length 100 bp 
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of 776 bp in length
100 bp
of 681 bp in length
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8: gap of 100 bp
3005: contif 100 bp
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of 679 bp in length
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682 bp in length
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of 682 bp in length
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of 755 bp in length
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contig of 675 bp in length
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11840: gap of
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11070 11740: cont
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6290: con
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10969: con
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9409: co
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7853: cc
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1391: cc
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Lutect Submission

Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Sa (bases 1 to 65851)

Barran, N., Bastien, V., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cook, A., Cook, A., Fitzerala, M., Gage, D., Galagan, J., Farolis, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Lavine, R., Lindblad-Toh, K., Liu,G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Narder, M., Marphy T., Maylor, J., Meneus, L., Milnova, Y., Meterson, K., Murphy T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., Phunkhang, P., Pierre, M., Raymond, C., Retta, R., Rise, C., Royov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Sepencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Vel, R., Vo, A., Wilson, B., Wux, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
Meneus, L., Minova, T., Midenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rettas, R., Rieback, M., Riley, R., Rise, C., Sqov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stopanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Traillo, J., Vossillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 30, 2002 this sequence version replaced 91:21699374.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://fp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   will be sequenced to completion. In the event that
the record is updated, the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
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13: gap of
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Center clone name: 519_0_19
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4914 555
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JOURNAL
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens chromosome 17 clone RP13-519019 map 17, LOW-PASS
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                                                                                      g of 658 bp in length
100 bp
g of 666 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49: gap of 100 bp
50338: contig of 689 bp in length
138: gap of 100 bp
51107: contig of 669 bp in length
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47187: contig of 677 bp in length
                                                                                                                                                                                                                     oof 100 bp
contig of 656 bp in length
oof 100 bp
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27: contig of 675 bp in length
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665 bp in length
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664 bp in length
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of 680 bp in length
            in length
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Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP13-519019
      41784: contig of 681 bp
84: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                        683 bp
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46410: contig of
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49549: contig
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52651: contig
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44096: contig
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44852: con+
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48012: cr
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                                                                                                                                                                                                                                                                                                                                                                                  77 9066; gap of 100 bp 100 bp 9714; contig of 648 bp in length 15 9814; gap of 100 bp 10534; contig of 720 bp in length 15 10634; gap of 100 bp 100 bp 1148; gap of 100 bp 1148; gap of 100 bp 1148; gap of 100 bp 115160; contig of 712 bp in length 12160; contig of 712 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 13916; gap of 100 bp
18 14633; contig of 717 bp in length
19 14643; contig of 717 bp in length
19 1546; contig of 713 bp in length
17 15546; gap of 100 bp
17 16272; contig of 726 bp in length
18 16772; app of 100 bp
18 17715; contig of 743 bp in length
                                                                                contig of 100 bp contig of 727 bp in length p of 100 bp contig of 734 bp in length
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34433: contig of 738 bp in length
35376: contig of 743 bp in length
35376: contig of 743 bp in length
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2 (bases 1 to 80669)
Wu,H., Lin,S., Jia,H., Dutcher,S. and Roe,B.A.
Direct Submission
Submitted (14-AuG-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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* This sequence will be replaced * This sequence will be replaced * by the finished sequence as soon as it is available and
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44359: contig of 738 bp in length
44459: gap of 100 bp
45298: gap of 100 bp
45298: gap of 100 bp
4611: contig of 713 bp in length
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46112 46840: contig of 729 bp in length
46841 46940: gap of 100 bp
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1 (bases 1 to 80669)
14. Lib.S., Jia,H., Dutcher,S. and Roe,B.A.
Chlamydomonas reinhardtii BAC Clone cr-1j6
                                                                                                         in
5 36224: gap of 100 bp

5 36946: contig of 722 bp ir

7 37046: gap of 100 bp

7 37776: contig of 730 bp ir

7 37876: gap of 100 bp

8 38577: contig of 701 bp ir

8 38677: gap of 100 bp
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Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
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Homo sapiens chromosome 16 clone RPl1-13M21, LOW-PASS SEQUENCE
SAMPLING.
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DoE Joint Genome Institute.

Direct Submission

Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Jan 26, 2000 this sequence version replaced gi:5686044.

Center: Joint Genome Institute
                                             1...80669
/organism="Chlamydomonas reinhardtii"
/db_xref="taxon:3055"
/clone="cr-1j6"
/clone_lib="cr-1j6"
/note="This is one of two clone in the same well cr-1j6"
a 25825 c 24793 g 15894 t 3 others
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Catarrhini; Hominidae; Homo.
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* the accession number will be preserved.
* 1 80669: contig of 80669 bp in length.
Location/Qualifiers
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contig of 664 bp in length
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Mammalia; Eutheria; Primates; Cata
1. (bases 1 to 90280)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
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Web site: http://www.jgi.doe.gov
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30771 31473 32519 33730 33805 34776	36527 37179 38598 39400 40533 41612 42658 43645 46148 47218 48522 49310 50844	52194 53318 54464 55712 56684 58210 59764 61210 62916 64135 65999 67326 68611 70087
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8) of LMFLCHR12 from base 100001 (AL390114 Leishmania major chromc
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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0
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                                                                                                                                                   100.0%; Score 15; DB 2; Length 90280; 100.0%; Pred. No. 38;
                                                                                                                                                                                                                     0; Indels
74258: contig of 948 bp in length
gap of unknown length
75836: contig of 1578 bp in length
gap of unknown length
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710000
757191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence split into 8 fragments L Sequent Name En LMFLCHR12_0 100001 21 LMFLCHR12_1 200001 31 LMFLCHR12_3 300011 41 LMFLCHR12_4 400001 51 LMFLCHR12_5 500001 61
                                                                                                                                                                                                                                                                                                                Db 63309 CCTTCTCGCCCTGTT 63295
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Continuation (2 of
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LMFLCHR12_1
WPCOMMENT
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Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martin, R., Massey, E., Mawhiney, E., Machedd, H., Morbbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nuyen, A., Nguyen, N., Nguyen, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Paimus, E., Pu, L.L., Quh, M., Okwuonu, G., Craquny, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Sott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfcod, B., Thomas, N., Thomas, S., Warlen, R., Warden, K., Warden, K., Washington, C., Walliamson, A., Wallamson, R., Walliamson, A., Wallamson, R., Weinstock, G. and Gibbs, R., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Nerley, K., W., C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Direct Submission

AL Unpublished

SS Grand Gibbs, R., C., Chasses I to 150765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 65 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15624602.

Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 115371 bases at least Q40
Consensus quality: 123148 bases at least Q30
Consensus quality: 129020 bases at least Q30
Estimated insert size: 114258; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 1.6x in Q20 bases; sum-of-contigs estimation
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------ Summary Statistics
ASSembly program: Phrap; version 0.990329First call to
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16075)

Chu,T., Blumenfeld,M. and Cohen,D.

Biallelic markers derived from genomic regions carrying genes

Diallelic markers derived from genomic regions Carrying genes

Patent: WO 0151659-A 544 19-JUL-2001;

GENSET (FR)
                                                                                                                                                                                                                                                                                                               Gaps
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; Pred. No. 37;
0; Mismatches 0; Indels 0;
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          contig of 1808 bp in length.
gap of unknown length
contig of 1884 bp in length
gap of unknown length
contig of 1435 bp in length
gap of unknown length
contig of 1252 bp in length
gap of unknown length
gap of unknown length
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135794: contig of 1413 bp in length
135894: gap of unknown length
137173: contig of 1279 bp in length
13883: contig of unknown length
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length
bp in length
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of 1280 bp in length
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of 1579 bp in length
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34799. .34930
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                                                                                                                                                                                                                                                             unknown length
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1. 160755
7. organism="Homo sapiens"
Ad_xref="taxon:9606"
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7. orgalatory region"
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7. hote="exon 1"
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7. hote="exon 1"
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/note="99-32148-315.mis"
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7.0 21 AAC53876 7.1 22 ABA572837 7.1 22 ABA572837 7.1 22 ABA572837 7.1 22 AAK15595 7.1 22 AAK15595 7.1 22 AAK15744 7.1 22 AAK1574 7.1 22 AAK1574 7.1 22 AAK1574 7.1 22 AAK1574 7.1 22 AAK1593 80 20 AAX24591 81 22 AAK10609 82 AAK10609 83 22 AAK10609 84 22 AAK10609 89 22 AAK10609 89 22 AAK16609 89 22 AAK16771 89 22 AAK16609 89 22 AAK1673 89 22 AAK16609 89 22 AAK1673 89 22 AAK16609 89 22 AAK1673 80 22 AAK1675 80 22 A	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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7.11.11.11.4.4.6.7.4.8.8.8.8.8.8.8.8.8.8.8.8.8.8.8.8.8.8	33.3 33.3 33.3 33.3 33.3 33.3 33.3 33.3 33.3 33.3 33.3 34.0 35.0 36.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0 37.0
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The present sequence represents a probe for the wild type allele of a human norepinephrine transporter gene. The specification a method for susceptibility to sub-optimal norepinephrine transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism norepinephrine transport. The method is useful for screening for susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of subject to rethostatic intolerance. Norepinephrine transporter genes are useful for gene therapy for modulating norepinephrine transport in a target cell and treating susceptibility to impaired norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, hypertension, heart disease, psycho stimulant abuse e.g. cocaine or
                                                                                                              Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene
                                                                                                                                                                                                   Claim 15; Page 69; 133pp; English.
                             Blakely RD;
                                                                     WPI; 2001-425681/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amphetamine abuse.
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                             Robertson D,
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                                                                                         MAGE-21 gene.
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ABQ41086
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    05-SEP-2001 (first entry)
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6932
6937
7057
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7111
7114
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C 984
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9959
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                                                                                                                                                                                                                                   Single nucleotide polymorphism; SNP; biallelic marker; human; ds; central nervous system disorder; CNS; NET; norepinephrine transporter.
                                            Gaps
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/standard_name= "single nucleotide polymorphism"
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0
                     Length 15;
                                            Indels
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0
                    100.0%; Score 15; DB 22; 100.0%; Pred. No. 11;
Sequence 15 BP; 0 A; 7 C; 2 G; 6 T; 0 other;
                                          Mismatches
                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                            AAH88259 standard; DNA; 920 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                       13-JAN-2000; 2000US-0175854
                                                                                                                                                                                         (first entry)
                              Best Local Similarity 100.
Matches 15; Conservative
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                                                                            CCTTCTCGCCCTGTT
                                                                 1 CCTTCTCGCCCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEST ) GENSET.
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28-DEC-2000; 2000WO-US35491 29-DEC-1999; 99US-0173682. 11-JAN-2000; 2000US-0175456.

(UYVA-) UNIV VANDERBILT.

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Homo sapiens.
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11-JAN-2000;
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                                                     The present invention relates to biallelic markers derived from human genes involved in central nervous system (CNS) disorders. The present sequence is one such biallelic marker derived from human norepinephrine transporter (NET) gene. This marker has a single nucleotide polymorphism (SNP) and is useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set of genetic markers in a biological sample, where the markers comprise at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to biallelic markers derived from human genes involved in central nervous system (CNS) disorders. The present sequence is one such biallelic marker derived from human norepinephrine transporter (NET) gene. This marker has a single nucleotide polymorphism (SNP) and is useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set of genetic markers in a biological sample, where the markers comprise at least one CNS disorder related marker.
                                                                                                                                                                                                                                                                                                                                                                                                                  Single nucleotide polymorphism; SNP; biallelic marker; human; ds; central nervous system disorder; CNS; NET; norepinephrine transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polynucleotides, useful for genotyping nucleic acids for biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker -
biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker -
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/standard_name= "single nucleotide polymorphism"
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                                                                                                                                                                                       100.0%; Score 15; DB 23; Length 920; 100.0%; Pred. No. 10;
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                                                                                                                                                                 Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents exon 9 of the human norepinephrine transporter gene. The specification a method for screening for susceptibility to sub-optimal norepinephrine (NE) transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to cuthostatic intolerance. Norepinephrine transport in a target cell and treating susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine;
                                                                                                                            Gaps
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                                                              23; Length 920;
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Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;
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                                                                                                                         Mismatches
                                                        Score 15;
Pred. No.
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2000US-0175456.
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                                                           Query Match
Best Local Similarity
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Length 1044;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapphing, and in recombinant production of (II). The and gene mapphing, and in recombinant production of (II). The polymerlectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques or restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and and and active and or produce other types of the invention.

Cuanno acid sequences. Ask64197-Ask94664 represent novel human diagnostic coding sequences of the invention.

Cuanno acid sequences of the invention.

Specification, but was obtained in electronic format directly from MIPO at the printed and product the printed and active active and active and active active and active active and active active active active active active active and active a
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                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                         .;
                                                                 Length 980;
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and
Sequence 980 BP; 218 A; 275 C; 246 G; 238 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #16550.
                                                                                                                   0
                                                           ch 100.0%; Score 15; DB 22; Si Similarity 100.0%; Pred. No. 10; 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 16550; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                             AAS80746 standard; cDNA; 1044 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-FEB-2002 (first entry)
                                                                                                                                                                                                         230 CCTTCTCGCCCTGTT 244
                                                                                                                                                                         1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73.
P-PSDB; ABG16559.
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                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS80746;
                                                              Query Match
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AAS80746/c
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Sequence 1044 BP; 229 A; 303 C; 258 G; 254 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine; amphetamine abuse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene
                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of a human norepinephrine transporter.
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "norepinephrine transporter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stimulant abuse e.g. cocaine or amphetamine abuse.
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   100.0%; Score 15; DB 23; 100.0%; Pred. No. 10;
                                                                            Mismatches
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1..1854
                                                                                                                                                                                                                                                                                                                                                                        AAH28082 standard; DNA; 1854 BP.
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Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                       1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                         97 CCTTCTCGCCCTGTT 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-425681/45.
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AAH28086

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Pools of clones from a human SK-N-SH cell (a human neuroblastoma cell line) cDNA library were transfected into COS-1 cells. The transfected clones were in the form of expression vectors (pXM) having an SV-40 replication origin to enable amplification.

Transfectants of these cells expressing the norepinepherine transporter were identified by employing an assay exploiting the fact that the norepinepherine analogue m-iodobersylguanidine (m-IBG) is accumulated intracellularly by SK-N-SH cells expressing the intact NT. The accumulated radiolabelled m-IBG allows direct autoradiographic visualisation of transporter expressing the intact NT. The accumulated radiolabelled m-IBG allows direct autoradiographic visualisation of transporter expressing the colone was obtd. Transfected from positive colonies and the resulting plasmid pools rescreened and subdivided until a single clone was obtd. Transfected cells become capable of norepinepherine uptake, which may be inhibited by various drugs, e.g. cocaine, to a degree similar to the effect of such drugs on noradrenergic neurons. The cloned cDNA makes possible well-controlled studies of neurotransmitter transporter function in non-neuronal cells same cell. Such studies include the relative effects of various
                                                                                                                                                                                                                                                                  NT; noradrenaline; neuroblastoma; neutotransmitter; antidepressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complementary DNA clone encoding human norepinephrine transporter protein - isolated from human neuroblastoma cells and useful for determining action of e.g. antidepressant drugs
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                                                                                                                                                                                                                   Human norepinepherine transporter protein cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           psychotropic) drugs such as antidepressants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pacholczyk T;
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                          AAQ28118 standard; cDNA; 1983 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-0676980.
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                                                                                                                                                                      15-MAR-1993 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                              61..1914
/*tag= a
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Best Local Similarity 100.
Matches 15; Conservative
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P-PSDB; AAR26416.
                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-1992;
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                                                      AAQ28118
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                                                                                                                                                                                                                                                                                                                                                         Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine; amphetamine abuse; ss.
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                                                                                                                                                                                                                                                                                                          Nucleotide sequence of a human norepinephrine transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "norepinephrine transporter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stimulant abuse e.g. cocaine or amphetamine abuse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 75; Page 112-115; 133pp; English.
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                                                                                                                                                               AAH28086 standard; DNA; 1854 BP.
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11-JAN-2000; 2000US-0175456.
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                                                                                                                                                                                                                                                           05-SEP-2001 (first entry)
                        1362 CCTTCTCGCCCTGTT 1376
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1 CCTTCTCGCCCTGTT 15
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mes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                              AAH28086;
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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by CGA, by detecting the level of expression of gene(s) (GS) identified by the expression level to an expression level in an unactivated CC the expression level to an expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent of that alters the expression of at least one gene in GS; (2) screening (M3) (M3) included are modulating (M2) GA by contacting GC with an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation of the gene is indicative of inflammation, or sterile inflammation with an agent that modulates the expression of gene(s) from GS. MA is useful for modulating GA; M3 is useful for screening an apple of modulating CGA preferably in an inflammation in a tissue; M4 is useful for exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic creening an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic or response in a subject, exposure of a subject to a pathogen or sterile ential man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                   viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                        Human cDNA differentially expressed in granulocytic cells #433.
                                                                                                                                                                                                                                                               granulocytic cell; DNA chip; bacterial infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 433; 114pp; English.
                                                    ABK83862 standard; cDNA; 5161 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beazer-Barclay Y, Weissman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2001; 2001WO-US30821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2000; 2000US-237189P.
                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-435328/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200228999-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                          14-AUG-2002
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                                                                                                     ABK83862;
RESULT 9
ABK83862/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to biallelic markers derived from human genes involved in central nervous system (CNS) disorders (see AAH88161-AAH88702). The markers have a single nucleotide polymorphism (SNP) and are useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set genetic markers in a biological sample, where the markers comprise at least one CNS disorder related marker. The present sequence was used to illustrate the invention.
                                                                                                                                                             Gaps
sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polynucleotides, useful for genotyping nucleic acids for biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 160755 BP; 43057 A; 36601 C; 38189 G; 42727 T; 181 other;
                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 15; DB 23; Length 160755; 100.0%; Pred. No. 8.7; 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                            Length 5161;
                                                                                                                                                                                                                                                                                                                                                                                                                             Single nucleotide polymorphism; SNP; biallelic marker; human;
                                                                                         Sequence 5161 BP; 1254 A; 1420 C; 1363 G; 1124 T; 0 other;
                                                                                                                                                        0; Indels
                                                                                                                     100.0%; Score 15; DB 24;
100.0%; Pred. No. 9.6;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            central nervous system disorder; CNS; ds.
                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 476-519; 519pp; English.
                                                                                                                                                                                                                                                                                               AAH88704 standard; DNA; 160755 BP.
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                                                                                                                                                                                                                                                                                                                                                                                              Human DNA sequence SEQ ID 544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JAN-2000; 2000US-0175854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2001; 2001WO-IB00116.
                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63345 CCTTCTCGCCCTGTT 63359
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                     1 CCTTCTCGCCCTGTT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blumenfeld M,
                                                                                                                                                                                                        2673 CCTTCTCGCCCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-483085/52.
                                                                                                                                  Best Local Similarity
Matches 15; Conserv
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200151659-A2.
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                                                                                                                                                                                                                                                                                                                                                              26-FEB-2002
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                                                                                                                                                                                                                                                                                                                               AAH88704;
                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                   RESULT 10
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RESULT 11

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27552 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder. In humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide syndrome associated with ORFX-associated disorders. ORFX polynucleotide creatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious attritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                                                                                                                                                                                                 hyperproliferative disorder; psoriasis; benign tumour; haemorrhage, degenerative disorder; osteoarthritis; neurodegenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascoular disease, diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reperfusion injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                 open reading frame; ORFX; gene therapy; cancer; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 336 BP; 61 A; 101 C; 109 G; 64 T; 1 other;
                                                                                                                                                     Human ORFX polynucleotide sequence SEQ ID NO:4669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID 4669; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.3%; SCOLE
100.0%; Pre
                  ABN18096 standard; cDNA; 336 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                                                                                                                                                       myasthenia gravis; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P
                                                                                                          24-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-106308/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200192523-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                           ABN18096;
ABN18096
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABD54131-ABD56305), and also encompasses polypeptides 90% identical and polyproclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynuclectides, antibodies against human ovarian antigens, and the use of ovarian antigen polynuclectides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and catainstic tumours of ovarian or breast origin, reproductive system clisorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., anaemia), cardiovascular disorders, increlated disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, autoimmune ophoritis, systemic lupus erythematosus), respiratory disorders, neurological disorders, anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polypeptides and polypeptides may also be used in screening for compounds which
                                                                                                                                                                                                                                                                                                                                                                           ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecules encoding novel ovarian polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                               Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                                                                                                                                                                                                                                             Human ovarian antigen HVVAW26 cDNA, SEQ ID NO:2083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 2083; 2922pp; English.
                                                                                                                                                               ABQ56203 standard; cDNA; 655 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-2001; 2001WO-US18569.
                                                                                                                                                                                                                                                              22-AUG-2002 (first entry)
2 CTTCTCGCCCTGTT 15
                        82 CTTCTCGCCCTGTT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurological diseases
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modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the

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Gaps

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0; Indels

Mismatches

Matches 14; Conservative

Query Match Best Local Similarity

Score 14; DB 24; Length 336; Pred. No. 40;

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Gaps

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Length 708 Indels

22;

DB .

93.3%; Score 14; DB 100.0%; Pred. No. 39; iive 0; Mismatches

0 other;

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Sequence 708 BP; 152 A; 212 C; 196 G; 148 T;
                                                               Conservative
                                 Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter JC,
                                                                                                                                                                                                               ABL11823;
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Matches
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                                                                                                                                                             RESULT 14
                                                                                                                                                                        ABL11823,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
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                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
         polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                        Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
and the
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                                                                                                                                            93.3%; Score 14; DB 24; Length 655; 100.0%; Pred. No. 39; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ochiai K,
identification of individuals and in forensic analysis,
                                                                                                                    Sequence 655 BP; 182 A; 168 C; 177 G; 116 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                               glutamicum coding sequence fragment SEQ ID NO: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                                                       499/c
AAH65499 standard; DNA; 708
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                                                                                                                                                                                                                                                                                                                                                                                                                      organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                   556 CTTCTCGCCCTGTT 543
                                                                                                                                                                                                    2 CTTCTCGCCCTGTT 15
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                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakagawa S,
Tateishi N,
                                                     invention.
                                                                                                                                                                                                                                                                                                                           AAH65499;
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                                                                                                                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention siscloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster expressed polynucleotide SEQ ID NO 29951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 29951; 21pp + Sequence Listing; English
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                                                                                                                                                                                           .823/c
ABL11823 standard; cDNA; 2036 BP.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster.
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1 CCTTCTCGCCCTGT 14
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AAQ14533

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The 20.5 gene, also referred to as Tea, identifies transcripts found in only a limited number of tissues. Tea transcripts are induced in splenocytes activated with the T cell mitogen ConA. Unlike other known genes expressed in activated T cells, the Tea gene appears to encode a protein which traverses the membrane multiple times, whereas the large number of known integral membrane protein which are induced in T cell activation are single membrane spanning proteins. See also AAQ14530-34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant polypeptide comprising a T-cell protein - used to regulate T-cell development and tumorigenic phenotype and to block T-cell activation in auto:immune disease
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                                                                                                            Multiple membrane spanning protein; T cell; development; ss.
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AAQ14533 standard; DNA; 2397 BP.
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                                                                                Tea gene (cDNA 20.5)
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GENERAL INFORMATION:

APPLICANT: MACLEGG Dr., Carol I.

TITLE OF INVENTION: No. 5440017el T-cell Lymphoma CDNA Clones
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Department, Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STREET: PatentIn Release #1.0, Version #1.25
COMPUTER READABLE FORM:
MEDIUM TIPE: PatentIn Release #1.0, Version #1.25
COMPUTER: PatentIn Release #1.0, Version #1.25
COMPUTER: IBM PC compatible
OPERATION SYSTEM: US/08/002,999
FILING SYSTEM: 19930111
CLASSIFICATION NUMBER: US 07/686,322
FILING DATE: 11930111
ATTORNEY APPLICATION NUMBER: US 07/686,322
FILING DATE: 11395
FILING DATE: 11395
FILING DATE: 11395
TELEPHONE: (713) 651-534
TELETRY: Western Union 762829
INFORMATION FOR EQL ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2397 base pairs
TYPE: NUCLEIC AND A LO MRNA
ORGENISM: MOUSE
CORGANISM: MOUSE
CORGANISM: MOUSE
CORGANISM: MOUSE
CORGANISM: MOUSE
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100'.0%; Pred. No. 3.5;
iive 0; Mismatches
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                         SL12 cell line
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INDIVIDUAL ISOLATE: SL12 cell line
; STRAIN: AKRI Jackson
; INDIVIDDAL ISCLATE: SL12 cell l
; TISSUE TYPE: Lymphoma
; CELL TYPE: T-cell
; CELL LINE: SL12.3 and SL12.4
; IMMEDIATE SOURCE:
; CLONE: 20.5
US-07-686-322A-5
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08002999; Patent No. 5440017; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE: Lymphoma CELL TYPE: T-cell CELL LINE: SL12.3 and SL12.4
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Best Local Similarity
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CLONE: 20.5
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                         Sequence 1
Sequence 1
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Patent No. 5312733
GENERAL INFORMATION:
APPLICANT: MacLeod Dr., Carol L.
TITLE OF INVENTION: No. 5312733el T-cell Lymphoma cDNA Clones
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Patent Department, Fulbright & Jaworski STREET: 1301 McKinney, Suit 5100 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNATE: 14285
COUNTRY: USA
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTION DATA:
APPLICATION NUMBER: US/07/686,322A
FILING DATE: 19910411
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/686,322A
FILING DATE: 13-APR-1990
ATTONEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/509684
FILING DATE: 13-APR-1990
                                                                                                                                                                                                      US-09-352-616A-470
US-08-160-861-2
US-09-513-007-1
US-08-542-363-3
US-09-100-089-3
US-09-670-827-3
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US-09-439-313-470
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US-09-624-693A-12
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US-08-922-182-1
US-08-919-953-1
US-09-192-983-1
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US-09-073-663-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Launer, Charlene A.
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: D-5232-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 651-3634
TELERA: (713) 651-5246
TELEX: Western Union 762829
INFORMATION FOR SEQ ID NO: 5:
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LENGTH: 2397 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-07-686-322A-5
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Length 2397;

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STATE: DC
COUNTRY: U
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                                            RESULT
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                                                                                                                                                                                                                                         APPLICANT: MERUELO, DANIEL
APPLICANT: YOSHIMOTO, TAKAYUKI
TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
    Gaps
    ;
0
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    Indels
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  ;
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: FLORPY disk
COMPUTER: FLORPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
PRICATION UNBER: US/08/132,990A
FILLING DATE: 07-OCT-1993
PRIOR APPLICATION DATA:
PRICATION DATA: 08/084,729
FILLING DATE: 29-JUN-1993
PRIOR APPLICATION DATA:
PRILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/806,178
FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/806,178
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/627,950
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MISSOCK, S. Leslie
                                                                                                                                                                                                                                                                                                                                                    IE: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                Sequence 5, Application US/08132990A Patent No. 5834589
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REFERENCE/DOCKET NUMBER: 810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFRAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2397 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 66441 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
  14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 100.
Matches 14; Conservative
                                                                              Db 1379 CTTCTCGCCCTGTT 1392
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STRANDEDNESS: single
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                                          2 CTTCTCGCCCTGTT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                               US-08-132-990A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-132-990A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                         STREET:
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Matches
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lee, Margie
APPLICANT: Sanchez, Susan
TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
TITLE OF INVENTION: Compositions and Diagnostic Methods
TITLE OF INVENTION: Compositions and Diagnostic Methods
FILE REFERENCE: 77-96B
CURRENT FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US/09/400, 208B
CURRENT FILING DATE: 1997-10-15
PRIOR FILING DATE: 1997-10-16
PRIOR FILING DATE: 1996-10-16
PRIOR FILING DATE: 1996-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                      APPLICANT: MERUELO, DANIEL
APPLICANT: YOSHIMOTO, TAKAYUKI
TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.3%; Score 14; DB 5; Length 2397; 100.0%; Pred. No. 3.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09382
FILING DATE: 19921213
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MERUELO=1
                                                                                                                                                                                                                                                                                                                                        ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
                                                                                                                                                                                                                     ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
PCT-US92-09382-5; Sequence 5, Application PC/TUS9209382; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/09400208B Patent No. 6271011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/CDCKET NUMBER: MERU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-5197
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1996-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2397 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , NAME/KEY: CDS
; LOCATION: 410..1768
PCT-US92-09382-5
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                                                                                                                                                                                                                                                                                                                       USA
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US-09-400-208B-22/c
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Gaps

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Sequence 6, Application US/09491522
Patent No. 6428998
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Colige, Alain
APPLICANT: Lapiere, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Lee, Margie
APPLICANT: Sanchez, Susan
APPLICANT: Henk, Adam
TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
TITLE OF INVENTION: Compositions and Diagnostic Methods
FILE REFERENCE: 77-968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2001;
                                                                                                                                                        86.7%; Score 13; DB 4; Length 497; 100.0%; Pred. No. 15; 0; Indels Live 0; Mismatches 0; Indels
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14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/400,208B
CURRENT FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 08/951,984
PRIOR FILING DATE: 1997-10-15
PRIOR FILING DATE: 1997-10-16
PRIOR FILING DATE: 1996-10-16
PRIOR FILING DATE: 1996-10-15
PRIOR FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATCHIN UND ST. 20
SOFTWARE: PATCHIN VET. 2.0
SECTION OF SEQ ID NOS: 27
LENGTH: 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09400208B Patent No. 6271011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Pasteurella multocida
                                                                  TYPE: DNA ORGANISM: Pasteurella multocida
Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                            Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                            464 CTTCTCGCCCTGT 452
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; NAME/KEY: mat_peptide
; LOCATION: (251)...(1486)
US-09-400-208B-4
                                                                                                                                                                                                                                                     2 CTTCTCGCCCTGT 14
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US-09-400-208B-4/c
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                                                                                                               US-09-400-208B-24
                     SEQ ID NO 24
LENGTH: 497
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SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lee, Margie
APPLICANT: Sanchez, Susan
APPLICANT: Sanchez, Susan
APPLICANT: Henk, Adam
TITLE OF INVENTION: Compositions and Diagnostic Methods
TITLE OF INVENTION: Compositions and Diagnostic Methods
FILE REPERENCE: 77-96B
CURRENT APPLICATION NUMBER: US/09/400,208B
CURRENT FILING DATE: 1999-09-21
PRIOR FILING DATE: 1999-09-21
PRIOR FILING DATE: 1996-10-15
PRIOR PILING DATE: 1996-10-16
PRIOR APPLICATION NUMBER: US 60/028,482
PRIOR FILING DATE: 1996-10-16
PRIOR FILING DATE: 1996-10-15
NUMBER OF: SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-400-208B-24/C

Sequence 24, Application US/09400208B

Patent No. 6271011

SERENAL INFORMATION:

APPLICANT: Lee, Margie

APPLICANT: Eac, Margie

APPLICANT: Banchez, Susan

APPLICANT: Henk, Adam

TITLE OF INVENTION: Compositions and Diagnostic Methods

FILE REFERENCE: 77-96B

CURRENT APPLICATION NUMBER: US/09/400,208B

CURRENT FILING DATE: 1999-09-21

PRIOR APPLICATION NUMBER: US 60/028,876

PRIOR APPLICATION NUMBER: US 60/028,876

PRIOR APPLICATION NUMBER: US 60/028,876

PRIOR APPLICATION NUMBER: US 60/028,482

NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                86.7%; Score 13; DB 4; Length 485; 100.0%; Pred. No. 15; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/09400208B Patent No. 6271011
                                                                                        TYPE: DNA ORGANISM: Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Pasteurella multocida
US-09-400-208B-23
                       Patentin Ver. 2.0
                                                                                                                                                                                                       Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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414 CTTCTCGCCTGT 402
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NUMBER OF SEQ ID NOS:
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Lee, Ma
                                                                                                                                                                                                                                                                                                                                                                                                          US-09-400-208B-23/C
                                                                                                                                     US-09-400-208B-22
                     SOFTWARE: Pat
SEQ ID NO 22
LENGTH: 485
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LENGTH: 491
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DESHYDROGENASE, -N.ACETYLHEXOSAMINIDASE
AND -ACTIN AND THEIR USE IN FILAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: READELE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
SOFTWARE: WordPerfect 8 for Windows
                                                                                                                                                                                                                                                             Score 13; DB 4; Length 2450; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (C) REF./DOCKET NO.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BARREDO FUENTE, Jose Luis
RODRIGUEZ SAIZ, Marta
COLLADOS DE LA VIEJA, Alfonso J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/ES98/00056
FILING DATE: 5-MAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: 5-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,337A
FILING DATE: 14-May-1999
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORENO VALLE, Migeul Angel
SALTO MALDONADO, Francisco
DIEZ GARCIA, Bruno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MASS, Clifford J. REGISTRATION NUMBER: 30,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 4, Application US/09171337A
; Patent No. 6300095
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             86.7%; ;
100.0%;
                 TELEPHONE: 650-493-4935
TELEFAX: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2450 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2(CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleotides
                                                                                                                                                                                                                                                        Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                      511 CCTTCTCGCCCTG 499
                                                                                                                                                                                                                                                                                                                                             1 CCTTCTCGCCTG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO
                                                                                                                                                                                              ; TOPOLOGY: linear
US-09-491-522-2
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APPLICANT: Lapiere, Charles M.
APPLICANT: Lapiere, Charles M.
APPLICANT: Brockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds, LLP
STREET: LISS Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                OPERATING STERM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
FILING DATE:
FILING DATE:
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OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
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REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-0060-999
                                                                                                                                                                                                                                                                                                                                                                 8389-0900-688
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APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEXX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
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Patent No. 6428998
GENERAL INFORMATION:
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COUNTRY,
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2023 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   511 CCTTCTCGCCCTG 499
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US-09-491-522-6
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Les 13; Conserv
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COUNTRY:
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Matches
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U-011948-3

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/label= actin_gene
/note= "Nucleotide sequence of region B in Figure
60. Sequence corresponds to Figure 62."
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Patent No. 6090607
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: ENHANCED EXPRESSION OF
TITLE OF INVENTION: PROTEOLYTIC ENZYMES IN KOJI MOLDS
NUMBER OF SEQUENCES: 17
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/254,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(1294..1300, 1428..1458, 1631..1686, 1797
..1827, 1918..2689, 2757..2984)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.7%; Score 13; DB 100.0%; Pred. No. 14; tive 0; Mismatches
           LENGTH: 3748 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Acremonium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
SEQUENCE CHARACTERISTICS:
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1428..1458
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1797..1827
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2757..2984
                                                                                                                                                  NAME/KEY:
- NAME/KEY:
- LOCATION: 1..3748
- OTHER INFORMATION:
- OTHER INFORMATION:
- OTHER INFORMATION:
- FEATURE:
- NAME/KEY: exon
- LOCATION: 1294..1306
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NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
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APPLICANT: Zushi, Komakazu
APPLICANT: Gomi, Komakazu
APPLICANT: Yamamoto, Shuji
APPLICANT: Watsuda, Akio
TITLE OF INVENTION: A Polypeptide Capable of Interacting
TITLE OF INVENTION: with Thrombin
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,206A
                                                                                                                                                                                                                                                                                                                                                                                                            86.7%; Score 13; DB 4;
100.0%; Pred. No. 14;
tive 0; Mismatches C
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         ORGANISM: Penicillum chrysogenum IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                    LOCATION: 2183...2249
CHER INFORMATION: act gene
SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-171-337A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Svensson, Leonard R. REGISTRATION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 216-275P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,492
FILING DATE: 03-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-261-206A-76/c
; Sequence 76, Application US/08261206A
; Datent No. 5574007
; GENERAL INFORMATION:
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794...920
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INFORMATION FOR SEQ ID NO: 76:
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TELEFAX: 703-241-2848
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Best Local Similarity 100..
                                                 CLONE: <Unknown>
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ORIGINAL SOURCE:
                                                                                     NAME/KEY:
LOCATION:
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                                                                                                                                                           LOCATION:
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Sequence 1, Application US/08319387
Patent No. 5543317
GENERAL INFORMATION:
APPLICANT: Shields, Malcolm S.
APPLICANT: Francesconi, Stephen C.
TITLE OF INVENTION: Microbial Degradation of Trichloroethylene, TITLE OF INVENTION: Dichloroethylenes and Aromatic Pollutants NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/319,387
                                                                                                                                                                                                                                                                                                                                                                     E: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/167,457
FILING DATE: 15-DEC-1993
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/694,718
FILING DATE: 02-MAY-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.7%; Score 13; 100.0%; Pred. No.
   Best Local Similarity 100.0%; P
Matches 13; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UWI
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TELEPHONE: 904-375-8100
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LENGTH: 9785 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: FL.
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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                                                                               511 CCTTCTCGCCCTG 499
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                                                             1 CCTTCTCGCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                      RESULT 15
US-08-319-387-1/C
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APPLICANT: Colige, Alain
APPLICANT: Lapiere, Charles M.
APPLICANT: Lapiere, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                            /label= TRUNCATED-AREA
/note = "AREA IS TRUNCATED IMMEDIATELY
DOWNSTREAM THE SEQUENCE ENCODING
A DNA BINDING DOMAIN"
                                                                                                                                                                                                                                                                                                                               Length 4657;
                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                               DB 3;
14;
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APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-0060-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 661-41 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARCTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                               Score 13;
Pred. No.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
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US-09-491-522-1/c
; Sequence 1, Application US/09491522
; Patent No. 6428998
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COMPUTER: IBM Compatible
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APPLICANT: Boehringer Ingelheim Pharma KG
APPLICANT: Boehringer Ingelheim Pharma KG
TITLE OF INVENTION: Method for identifying substances which positively
TITLE OF INVENTION: influence influence influence of influence influence influence influence influence of influence influence influence influency airway diseases
FILE REFERENCE: 082_00n
CURRENT APPLICATION NUMBER: 08/09/44,807
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: UK 0021484.1
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10 US-09-864-711-4
10 US-09-964-456-1166
10 US-09-815-242-67
10 US-09-815-242-656
10 US-09-815-242-456
10 US-09-814-136
10 US-09-814-136
10 US-09-815-242-4147
10 US-09-815-242-4147
10 US-09-815-242-4147
10 US-09-781-77-10
10 US-09-791-17-17
10 US-09-791-17-17
10 US-09-791-17-17
10 US-09-791-17-17
10 US-09-79-307-19
10 US-09-815-242-7963
10 US-09-816-242-7963
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10 US-09-919-781-1
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US-09-880-107-3407
US-09-967-768A-190
US-09-887-576-38
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US-09-764-878-258/c
S. Sequence 258, Application US/09764878
; Patent No. US20020090615Al
; GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
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; ORGANISM: Homo sapiens
US-09-944-807-9
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Sequence 1. Application US/09430029
Patent No. US20020168738A1
GENERAL INFORMATION:
TOTAL OF INVENTION:
TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,
TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,
TITLE OF INVENTION: Compounds and Aromatic Compounds, and
TITLE OF INVENTION: Method for Environmental Remediation
FILE REFERENCE: CF013982US
CURREMY PFLING DATE: 1999-10-29
EARLIER APPLICATION NUMBER: JP P1998-310801
EARLIER FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1.
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Fatent No. US2002004953A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
PRIOR TAPLICATION OF EMPORED TEMPORED ACIDS TEMPORED ACI
                   TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA121
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 428
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Burkholderia cepacia
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US-09-764-878-258
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APPLICANT: Rosen et al
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Best Local Similarity
Matches 13; Conserv
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Matches 13; Conserv
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US-09-764-860-937/c
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LENGTH: 4558
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL PITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

N: EXPRESSED IN BRAIN, SIGNAL = 2.3

N: EXPRESSED IN PLACENTA, SIGNAL = 1.6

N: EXPRESSED IN PLACENTA, SIGNAL = 1.5

N: EXPRESSED IN PLACENTA, SIGNAL = 1.4

N: EXPRESSED IN BONE MARROW, SIGNAL = 2.1

N: EXPRESSED IN HBLIOO, SIGNAL = 1.4
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SEQ ID NO 17150
LENGTH: 152
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  Mismatches
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Patent No. US20020048763A1
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12; Conservative
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                                                    1 CCTTCTCGCCCT 12
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OTHER INFORMATION:
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US-09-864-761-17150
Matches
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APPLICANT: Huang, Qian
APPLICANT: Richmond, Joan F.L.
APPLICANT: Cho, Bryan K.
APPLICANT: Cho, Bryan K.
APPLICANT: Cho, Bryan K.
APPLICANT: Palliser, Deborah
APPLICANT: Palliser, Deborah
APPLICANT: Eisen, Herman N.
APPLICANT: Eisen, Herman N.
APPLICANT: Fisen, Herman N.
TITLE OF INVENTION: CD4+T Cell-Independent
FILE REFERENCE: 0399, 2006-003
CURRENT APPLICATION NUMBER: US/09/761,534A
FRIOR APPLICATION NUMBER: US 60/176,143
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-11-4
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Pred. No. 9.9;
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SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-761-534A-17
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Best Local Similarity 100.
Matches 13; Conservative
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LOCATION: (1495)..(1761)
OTHER INFORMATION: tomM
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OTHER INFORMATION: tomO
                                                 LOCATION: (234)..(443)
OTHER INFORMATION: LOMK
                                                                                                                         NAME/KEY: CDS
LOCATION: (463)..(1455)
OTHER INFORMATION: tomL
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LOCATION: (3810)..(4871.
OTHER INFORMATION: LOMP
FEATURE:
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Best Local Similarity
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LOCATION: (342
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LOCATION: (48)
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US-09-761-534A-17
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LENGTH: 49
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Sequence 5128, Application US/09983965
; Patent No. US20020137160A1
; GRNERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Warthon, Wesley C.
; APPLICANT: Wathialagan, Nagappan
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MSCLE AND FAT DEPOSITION
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 5128
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Sequence 5624, Application US/09867701

Sequence 5624, Application US/09867701

Sequence 5624, Application US/09867701

Sequence 5624, Application US/09867701

SEMERAL INFORMATION:

APPLICANT: Aplate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 80.0%; Score 12; DB 10; Length 380; Best Local Similarity 100.0%; Pred. No. 45; Matches 12; Conservative 0; Mismatches 0; Indels
                                                    80.0%; Score 12; DB 10; Length 235; 100.0%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: 33-LIB34-055-Q1-E1-A2 US-09-983-965-5128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%; Score 12; DB 10;
100.0%; Pred. No. 45;
iive 0; Mismatches 0
                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 80.0
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                 Conservative
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216 CTTCTCGCCCTG 205
                                                                                                                                            2 CTTCTCGCCCTG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Bos taurus
                                                 Query Match
Best Local Similarity
Matches 12; Conserv
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         US-09-923-876-97
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APPLICANT: Lalgudi, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: 05/09/923,876
CURRENT PAPPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SEQ ID NO 97
LENGTH: 235
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700142552H1
                                                                                                                                     80.0%; Score 12; DB 10; Length 152;
100.0%; Pred. No. 46;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 173; 46;
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-02
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR PLICATION NUMBER: 60/279,526
PRIOR PLING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTMARE: FASISEQ for Windows Version 4.0
    EXPRESSED IN FETAL LIVER, SIGNAL = 1.4 EXPRESSED IN LUNG, SIGNAL = 2 NT HIT: ALL163303.2, EVALUE 1.00e-80 SWISSPROT HIT: 060241, EVALUE 4.00e+00
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100.0%; Pred. No. 46;
tive 0; Mismatches
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Patent No. US20020013958A1
                                                                                                                                                                                    12; Conservative
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US-09-974-300-7193
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Best Local Similarity 100.
Matches 12; Conservative
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CTHER INFORMATION: E
COTHER INFORMATION: E
COTHER INFORMATION: CTHER INFORMATION: US-09-864-761-17150
                                                                                                                                       Query Match
Best Local Similarity
Matches 12; Conserv
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US-09-974-300-7193/c
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LENGTH: 173
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TITLE OF INVENTION: Brocess for Identifying Anti-Cancer Therapeutic Agents Using TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689280-77
CURRENT APPLICATION UNMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-22
SPRIOR FILING DATE: 2000-09-22
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                                DB 10; Length 396;
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                                                                                              0; Mismatches
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                                80.0%; Score 12; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                              Sequence 880, Application US/09954531
Patent No. US20020165180A1
GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
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                                                                 Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                283 CTTCTCGCCCTG 272
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US-09-954-531-880/c
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                                   Query Match
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APPLICANT: Rank David R.

APPLICANT: Rank David R.

APPLICANT: Rank David R.

APPLICANT: Rank David R.

APPLICANT: Hancal, David R.

APPLICANT: Hancal, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TILE REFERENCE: Accond.ca.x-1

CURRENT APPLICATION NUMBER: US/09/864,761

PRIOR FILING DATE: 2000-02-04

PRIOR PLICATION NUMBER: US 60/207,456

PRIOR PLICATION NUMBER: US 60/207,456

PRIOR PLILING DATE: 2000-00-04

PRIOR PLILING DATE: 2000-00-04

PRIOR PLILING DATE: 2000-00-07

PRIOR PLILING DATE: 2000-10-04

PRIOR PLILING DATE: 2001-01-04

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N: EXPRESSED IN HEART, SIGNAL = 2.9

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3

N: EXPRESSED IN BT474, SIGNAL = 1.4

N: EXPRESSED IN BUT74, SIGNAL = 2.2

N: EXPRESSED IN HELA, SIGNAL = 2.7

N: EXPRESSED IN HELLO, SIGNAL = 3.5

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8

N: EXPRESSED IN BRAIN, SIGNAL = 1.2

N: EXPRESSED IN LONG, SIGNAL = 3.9
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                   Sequence 3392, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
19 TCTCGCCCTGTT 30
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COTHER INFORMATION: E.
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FACENT NO. US.CUOLUD.180A1

FACENT NO. US.CUOLUD.180A1

APPLICANT: Weaver, Zoe

TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C

TITLE OF INVENTION: Gene Sets

FILE REFERENCE: 689290-77

CURRENT APPLICATION NUMBER: US/60/233,133

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-22

PRIOR FILING DATE: 2000-09-22

SOUTHWARE PAPLICATION NUMBER: US/60/234,567

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 1392

SOFTWARE PATENT APPLICATION NUMBER: US/60/234,567

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 1392

SEQ ID NO 813

LENGTH: 461
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45;
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           COMPUTER: Diskette - 3.5 inch, 1.44 Mb COMPUTER: IBM COMPALLIDE PC OPERATING SYSTEM: Windows 95 SOFTWARE: Word 97 (DOS text format) APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                        NAME: Grady J. Frenchick
REGISTRATION NUMBER: 29,018
REFERENCE/DOCKET NUMBER: 16026.9180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 257-3501
TELEFAX: (608) 257-2275
INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        APPLICATION NUMBER: US/09/784,423
FILING DATE: 15-Feb-2001
CLASSIFICATION: 4Uhknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 04-Feb-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.0%; Score 12; 100.0%; Pred. No.
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CLONE: G158
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MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 447 bp
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
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LOCATION: (1)...(461)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 CCTTCTCGCCCT 96
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US-09-954-531-813/c
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NN: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

NN: EXPRESSED IN BRAIN, SIGNAL = 2.3

NN: EXPRESSED IN HEART, SIGNAL = 1.8

NN: EXPRESSED IN HEART, SIGNAL = 1.5

NN: EXPRESSED IN BRAINAL = 1.5

NN: EXPRESSED IN BUT44, SIGNAL = 1.4

NN: EXPRESSED IN BUT41, SIGNAL = 2.1

NN: EXPRESSED IN HELOO, SIGNAL = 1.8

NN: EXPRESSED IN HETAL LIVER, SIGNAL = 1.8

NN: EXPRESSED IN LONG, SIGNAL = 1.8

NN: EXPRESSED IN LONG, SIGNAL = 1.4
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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Patent No. US20020012924A1
GENERAL INFORMATION:
APPLICANT: Schumm, James W.
Bacher, Jeffery W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
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COMMENT Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tal: 314 286 1800 Fax: 314 280 Fax: 316 280 Fax: 316 280 Fax: 316 280 Fax: 316 280 Fax: 310 280 Fa	Query Match Best Local Similarity 100.0%; Score 15; DB 14; Length 309; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 CCTTCTGGCCTGTT 15	RESULT 2 BH019102 LOCUS LOCUS LOCUS DEFINITION L2358k.d_HygT3.1 Leishmania major Friedlin Cosmid Genomic Library Leishmania major genomic clone L2358k, DNA sequence. Leishmania major genomic clone L2358k, DNA sequence. RENGION VERSION BH019102.1 GI:14197808 KEYWORDS GSS. SOURCE Leishmania major ORGANISM Leishmania major CRANISM Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;	REFERENCE 1 (bases 1 to 313) AUTHORS Myler,P.J., Vogt,C., Cawthra,J., Klacking,M., Marty,A., Mack,J., Munden,H., Wquyen,D., Robertson,E., Sisk,E., Fazelinia,G., Aggarwal,G., Nelson,S., Seyler,A., Worthey,E. and Stuart,K. TITLE Leishmania major Friedlin Cosmid End Sequences JOURNAL Unpublished (2000) CONMENT Seattle Blomedical Research Institute A Nickerson Street, Seattle, WA 98109-1651, USA Tel: 206 284-0313 Email: mylerpj@spri.org	Class: cosmid ends. FEATURES Location/Qualifiers 1. 313 Correct Abore="Leishmania major" //db_xref="taxon:564" //db_xref="taxon:564" //db_ref="taxon:564" //dboe="L2358k" //dboe="L2358k" //dboe="L2358k" //dboe="L2358k" //dboe="L255k" //dboe="L255k" //dboe="L255k" //dboe="L255k" //dboe="L255k"
BI530279 BI189550 BI189550 BI189550 BI189550 BI189550 f2c01fs.f BI192229 BI192229 m2b08fs.f BM189194 AQ505614 AQ5065138 AQ5065138 AQ5065138 AQ5065138 AQ5065138 AQ5065138 AQ5065138 AQ506655 AQ506655 AQ506655 AQ506655 AQ606655 AQ606655 AQ10306655 AQ10306655 AQ103041 AQ102031 AQ102031 AQ102031 AQ102031 AQ102031 AQ102031 AQ102031 AQ10311 AQ10311 BF197531 BF197531 AQ10331 AQ065745 AQ065745 AQ065745 AQ065745 AQ065744 AQ0667544 AQ		2835 FO 443612 BB 22650 AIG 7210 C9 5960 H4 32842 D4 119265 BE	148892 309 bp mRNA linear EST 06-FEB-1995 yb07a09.rl Stratagene placenta (#937225) Homo sapiens cDNA clone ALPHA 1(XV) CHAIN - HUMAN, mRNA sequence. 1748892 148892.1 GI:650752 EST. HOMO. Sapiens HOMO. Sapiens EUARTYOCE, METAZOA; Craniata; Vertebrata; Euteleostomi; BuARTYOCE, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	1 (bases 1 to 309) Hillier,L. Dennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags 97044478
12 80.0 306 13 BII 12 80.0 307 13 BII 12 80.0 307 13 BII 12 80.0 307 17 AQQ 12 80.0 308 10 BB8 12 80.0 308 10 BB8 12 80.0 308 9 AAQZ 12 80.0 309 9 AAQZ 12 80.0 310 10 BBII 12 80.0 310 10 BBII 12 80.0 310 10 BBII 12 80.0 311 13 BII 12 80.0 311 13 BII 12 80.0 311 13 BII 12 80.0 311 14 H24 13 80.0 312 14 H24 14 H24 15 80.0 313 12 BFII 16 80.0 312 14 H24 17 80.0 313 12 BFII 18 80.0 313 14 H24 18 80.0 313 12 BFII 19 80.0 313 BII 10 80.0 311 13 BII 11 80.0 311 13 BII 12 80.0 311 13 BII 13 80.0 311 13 BII 14 H24 15 80.0 313 12 BFII 16 80.0 313 12 BFII 17 80.0 313 12 BFII 18 80.0 313 12 BFII	80.0 317 99 80.0 317 10 80.0 317 10 80.0 317 10 80.0 317 10 80.0 318 10 80.0 318 14	80.0 318 14 FO 80.0 320 10 BB 80.0 321 14 C9 80.0 322 14 H4 80.0 322 14 H4 80.0 324 9 AI9 80.0 324 10 BE	T48892 yb07a09.rl Stratagene pla JMAGE:70456 5' similar to ALPHA 1(XV) CHAIN - HUMAN T48892 F48892. GI:650752 EST. human. HOMO sapiens Evaryota; Metazoa; Chord Mammalia; Eutheria; Prima	l (bases 1 to 309) Hiller, L., Lennon, G., Be Chissoe, S., Dietrich, N., 'M., Hultman, M., Kucaba, T., 'B., Morris, M., Parsons, J. 'Schellenberg, K., Soares, M. Underwood, K., Wohldmann, P. Generation and analysis o Genome Res. 6 (9), 807-82

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RESULT 1 T48892/c LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Jackson, Y. and Bowers, Y.
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Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 432.
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
/note="Vector: cLHYG; Site_1: BamHI; Genomic DNA from Leishmania major Friedlin was partially digested with Sau3AI. size selected, and ligated with BamHI-digested cLHYG cosmid vector DNA. 9216 clones were picked and arrayed. Library construction is described in Ivens et al., Genomics Research, 8:135-145 (1998). The CLHYG vector (Acc. No. CVUS9231) is described in Ryan et al, Gene, 131:145-150 (1993)"
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Other_ESTs: if28e01.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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/dev_stage="Adult"
/lab_host="DH10B"
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100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
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BM273267.1 GI:17966560
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Fax: 617-495-8557
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amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806, 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
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Myler, P.J., Vogr, C., Cawthra, J., Klacking, M., Marty, A., Mack, J.,
Munden, H., Ngyen, D., Robertson, L., Sisk, E., Fazelinia, G., Aggarwal
, G., Nelson, S., Seyler, A., Worthey, E. and Stuart, K.
Leishmania major Friedlin Cosmid End Sequences
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//lab_host="Vector: CLHYG; Site_1: BamHI; Genomic DNA from Leishmania major Friedlin was partially digested with Sau3AI, size selected, and ligated with BamHI-digested CLHYG cosmid vector DNA. 9216 clones were picked and arrayed. Library construction is described in Ivens et al., Genomics Research, 8:135-145 (1998). The CLHYG vector (Acc. No. CVU59231) is described in Ryan et al, Gene, 131:145-150 (1993).
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4 Nickerson Street, Seattle, WA 98109-1651, USA
Tel: 206 284-0313
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/clone="L2357k"
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Seg primer: HygT3
Class: cosmid ends.
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Best Local Similarity 100.0%;
Matches 15; Conservative 0;
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Contact: Myler PJ
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Unpublished (1999)
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Fax: 617-495-8557
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 551)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Emishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hiller, L., Marra, M., Pape, D., Wille, T., Marthi, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas,
M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Endocrine Pancreas Consortium
L Onpublished (2000)
Other_ESTS: if254008.11
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
                                                                        543 bp mRNA linear EST 23-AUG-2000 AV434035 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone PM037d06_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="PM037d06_r"
/clone_lib="Porphyra yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1125408.yl Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens CDNA clone IMAGE:5677479 5' similar to SW:CAIE_HUMAN P39059 COLAGEN ALPHA 1(XV) CHAIN PRECURSOR. [1]; "MRNA sequence."
                                                                                                                                                                                                                                                              Porphyra.
1 (bases 1 to 543)
Nikaido,I., Asamizu,E., Nakajima,M., Nakamura,Y., Saga,N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                           Porphyra yezoensis
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
                                                                                                                                                                                                                                                                                                                                 Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Porphyra yezoensis"
/strain="TU-1"
/db_xref="taxon:2788"
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Best Local Similarity 100.
Matches 15; Conservative
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52 CCTTCTCGCCCTGTT 66
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SOURCE

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/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA made by oligo-dT prining. Size selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hybrary.
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602272934F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4361024 5',
mRNA sequence.
BF971415
                                                                                                                                                                                                                        Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu) This sequence now available from the IMAGE consortium, for clone orders contact: info@image.lnl.gov High quality sequence stop: 414.
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 617)
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// Organism="Homo sapiens"
/db_ref="taxon:9606"
/clone=TIM6E:5677479"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
// Sex="Both"
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Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCS
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
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                                                                                                                                                                                            Email: dmelton@biohp.harvard.edu
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AA099915/c
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                                                                                                                                                             /clone_lib="NHH_MGC_84"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab.host="bH10B (phage-resistant).
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
primed, Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHLMGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zk87h09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE.489857 3' similar to SW:CAIE_HUMAN P39059 COLLAGEN ALPHA 1(XV AA10211)
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Hillier, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., S., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 867 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 453.
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0
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
Feas: 314 286 1800
Frax: 314 286 1810
Email: est@watson.wustl.edu
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/clone_lib="Soares_pregnant_uterus_NbHPU"
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Pred. No. 1.9e+02;
0; Mismatches 0;
http://image.llnl.gov
Plate: LLAM10003 row: c column: 09
                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4361024"
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/db_xref="GDB:3804444"
                                         High quality sequence stop: 614.
Location/Qualifiers
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/dev_stage="adult"
/lab_host="DH10B"
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Best Local Similarity 100.0%;
Matches 15; Conservative 0;
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AA102111.1 GI:1646031
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                                                                                     .617
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DEUKATYOTE: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 628)

1 (bases 1 to 628)

1 (bases 1 to 628)

Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, M., Hawkins, M., Hultman, M., Kucaba, T., Leay, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Onderwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zk87h09.rl Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone NmAGE:489857 5' similar to SW:CAlE_HUMAN P39059 COLLAGEN ALPHA 1(XV AA099915
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                                                                                                                           Not
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Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5'
                                                                                   double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the No and Eco RI sites of the modified pTT3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

179 c 161 g 166 t 4 others
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 867 and Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 492.
Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/clone_lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                        Indels
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100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Fax: 314 286 1810
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constructed by M. Fatima Bonaldo."

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/organism="Chlamydomonas reinhardtii"
/strain="cc-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized
), Lambda Zap II"
/note="Vector: pBluescript II SK'; Site_I: ECORI; Site_2:
/note="Vector: pBluescript II SK'; Site_I: ECORI; Site_2:
xhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4+ - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
Phys. 122: 127-135; TAP + H2C2 (1, 12, 24 hr).
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized The cDNA was directionally cloned into lambda
zap II (Stratagene) in the EcoRI (5') and XhoRI (3')
sites: pBluescript II SK- plasmids were excised from the
lambda ZAP clones by superinfection with Exassist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 751-866.
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Grossman, A., Chang, C. W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDermort, J. P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtid Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031
L Unpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Duke University
Duke University
Duke University
Fax: 919 613 8157
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantea; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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5 others
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0;
                                                    100.0%; Score 15; DB 9; I
ilarity 100.0%; Pred. No. 1.9e+02;
Conservative 0; Mismatches 0;
122
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nes 15; Conserv
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BESLISYS4 659 bp MRNA linear EST 26-OCT-2000 601147310F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162555 5',
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MY-12-B-02 PinfestansMY Phytophthora infestans CDNA, mRNA sequence.
BE776197
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                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 659)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM122 row: c column: 04

High quality sequence stop: 618.
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Kamoun, S., Hraber, P.T., Sobral, B.W.S., Nuss, D. and Govers, F.
Initial assessment of gene diversity for the oomycete pathogen
Phytophthora infestans based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
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Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
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100.0%; Pred. No. 1.9e+02;
iive 0; Mismatches 0;
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/organism="Homo sapiens"
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Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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BQ609181
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/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/tab_most="bull0B (phage-resistant)"
/lab_most="bull0B (phage-resistant)"
/note="Organ: brain; Vector: poTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGGG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
                                                                                                                                                                                                                                                            Morellum in synthetic medium"

/lab_host="E. coli, strain DH5-alpha"

/note="Vector: pSpORTI; Site_1: Sall; Site_2: NotI; Total

/note="Vector: pSpoRTI; Site_1: Sall; Site_2: NotI; Total

RNA was isolated from mycellum of P. infestans DDR7602

cultured for 4 weeks in synthetic medium. EST clones were

named by their position in the microtiter plate, preceded

by the prefix MY (for mycellal) and the successive number

of the microtiter plate (e.g. MY 06-A-04)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF315344 11H_MGC_19 Homo sapiens cDNA clone IMAGE:4135278 5',
                  Binechaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.nl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM1039 row: e column: 07
High quality sequence stop: 644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                            /strain="DDR7602, Al mating type"
//db_xref="taxon:4787"
//clone_lib="PinfestansMy"
/dev_stage="4-week old vegetative, non-sporulating
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 676;
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                                                                                                                                                       /organism="Phytophthora infestans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 15; DB 12;
100.0%; Pred. No. 1.9e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                Location/Qualifiers
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Wageningen University
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Matches 15; Conserv
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TITLE
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KEYWORDS
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BRY_5105 wheat EST endosperm library Triticum aestivum cDNA 5', mRNA sequence. BQ609181. GI:21558520 EST.
                                                                                                                                                                                                                                                                            GA_Ea0025P19f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0025P19f, mRNA sequence.

BG444893.1 GI:13354545
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An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (báses 1 to 830)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="AKA"
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/db_xref="taxon:99729"
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/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
                                                                                                                      Gaps
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116 t
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                                                                           Length 713;
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Note: this is a NIH_MGC Library."
169 c 203 g 152 t
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Pred. No. 2e+02;
Mismatches 0;
                                                                                              Pred. No. 1.9e+02;
                                                                         100.0%; Score 15; DB 12; 100.0%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 Jordan Hall, Člemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University Genomics Institute
                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 182.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. coli"
                                                                                                                  0;
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Gossypium arboreum
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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
Triticeae; Triticum.
Triticeae; Triticum.
Sermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

I (bases 1 to 839)
SS Clarke, Lambrecht, M. and Rhee, S.
Assessing the utility of Arabidopsis genomic information for interpreting wheat EST sequences
In Umpublished (2002)
Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegle Institution of Washington, Dept. of Plant Biology
Zon Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 3748
Fax: 1 650 325 3748
Fax: 1 foo 325 1521 x 251
Fax: 1 coation/Qualifiers
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/organism="Triticum aestivum"
/cultivar="Wyuna"
/cultivar="Wyuna"
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/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
/note="Vector: Bluescript II SK(-)"
a 409 c 68 g 326 t
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0
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100.0%; Score 15; DB 14; Length 839;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels (
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AUTHORS
TITLE
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COMMENT
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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<pre>Run on: December 11, 2002, 12:26:07; Search time 1657 Seconds (without alignments) 263.453 Million cell updates/sec</pre>	Title: US-09-750-609-9 Perfect score: 15 Sequence: 1 ccttctcgccctgtt 15	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 2054640 segs, 14551402878 residues	Total number of hits satisfying chosen parameters: 4109280	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : GenEmbl:* 1: gb_ba:* 2: gb_ntg:* 3: gb_in:* 4: gb_om:* 5: gb_ow:* 7: gb_ph:* 8: gb_ph:*	
	December 11, 2002, 12:26:07	December 11, 2002, 12:26:07 US-09-750-609-9 15 1 ccttctcgccctgtt 15	December 11, 2002, 12:26:07 US-09-750-609-9 15 1 ccttctcgccctgtt 15 IDENTITY_NUC Gapop 10.0, Gapext 1.0	December 11, 2002, 12:26:07 US-09-750-609-9 15 1 cttctcgccctgtt 15 IDENTITY_NUC Gapop 10.0, Gapext 1.0 2054640 seqs, 14551402878 r	Run on: December 11, 2002, 12:26:07; Search time 1657 Seconds (without alignments) 263.453 Million cell updates/sec Perfect score: 15 Sequence: 1 ccttctcgccctgtt 15 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0 Searched: 2054640 seqs, 14551402878 residues Total number of hits satisfying chosen parameters: 4109280	, 12:26:07 15 1402878 r	, 12:26:07 15 15 51402878 r hosen para	, 12:26:07 15 15 1402878 r nosen para 08 summaries

gb_ro:*
gb_sy:*
gb_sy:*
gb_un:*
em_ba:*
em_fun:*
em_in:*
em_on:*
em_on:*
em_ov:*
em_ov:*
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em_htgo_other:*

is the number of results predicted by chance to have a Pred. No.

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 920)
Chu, T., Blumenfeld, M. and Cohen, D.
Biallelic markers derived from genomic regions carrying genes involved in central nervous system disorders

REFERENCE AUTHORS TITLE

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence	Score March Length DB ID Score March Length DB ID Maria 652 Score March Length DB ID Maria 652 Score March Length DB ID Maria 652 Score Maria 652 Maria 652 Score Maria 653 Maria 652 Maria 653 Maria 652 Maria 652 Maria 652 Maria 652 Maria 652 Maria 652 Maria 652			ø			SUMMARIES		
15 100 0 920 6 AX194629 AX194629 AX194629 15 100 0 920 6 AX194634 AX194639 BC000563 AX103434 AX10363 AX103634 AX103634 AX103634 AX103634 AX103634 AX103634 AX103634 AX103634 AX103634 AX10363 AX103634 AX103634 AX103634 AX103634 AX103634 AX10363 AX103634 AX1036	15 100 0 920	Result No.	Score	Query Match	Length	DB	ID	De	scription
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PRI 06-JUL-2001

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Direct Submission

L Submitted (30-AUG-195) H. Bonisch, Institut fuer Pharmacologie und Toxikologie, Universitetet Bonn, Reuterstr 2b, 53113 Bonn, FRG Related Sequences: M65105 and X57700.

Location/Qualifiers

I. .980 / Arganism="Homo sapiens" / Ab_xref="taxon:966" | About the component of the
                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi; Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 980)

Porzgen, P., Bonisch, H. and Bruss, M.
Molecular cloning and organization of the coding region of the Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. 215 (3), 1145-1150 (1995)
                                                                                                                                Homo sapiens partial SLC6A2 gene for norepinephrine transporter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 980)
Porzgen, P., Bonisch, H., Hammermann, R. and Bruss, M.
The human noradrenaline transporter gene contains multiple
polyadenylation sites and two alternatively spliced C-terminal
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norepinephrine transporter; SLC6A2 gene.
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/usedin=x91117:SLC6A2_mRNAa
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Bonisch, H.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Chu,T., Blumenfeld,M. and Cohen,D.
Biallelic markers derived from genomic regions carrying genes involved in central nervous system disorders
Patent: WO 0151659-A 104 19-JUL-2001;
                                                                                                                                                                                                                                                                                                                                           /66. 114
/note="16-2-76.mis2, complement"
240. 240. 70te="downstream amplification primer, complement"
1 260 c 225 g 227 t 4 others
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/note="downstream amplification primer, complement"
/note="downstream amplification primer, complement"
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100.0%; Pred. No. 6.6e+02;
ive 0; Mismatches 0; Indels
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                                                                             1. .920 /
/organism="Homo sapiens"
/db_xref="taxon:9606"
20. .39 /note="upstream amplification primer"
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/note="upstream amplification primer"
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Patent: WO 0151659-A 99 19-JUL-2001;
GENSET (FR)
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/note-"16-2-187.mis1"
194. .218
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/note="16-2-76.mis1"
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Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Gupta,J., Ho,S.-E., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 5 Row: i Column: 7
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KFDNNCYRDALLTSSINCITSFVSGFAIFSILGYMAHEHKVNIEDVATEGAGLVFILY
PEAISTLSGSTFWAVVFFVWLLALGLDSSMGGMEAVITGLADDFQVLKRHRKLFTFGV
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MMGRPGLIWRLCWREVSPAFLLFVVVVSIINFRPLTYDDYIFPPWANWVGWGIALSS
MVLVPIYVIYFLSTGGAAFALAYGITPENEHHLVAQRDIRQFQLQHWLAI"
378 c 376 g 373 t
                PRI 12-JUL-2001
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                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                         Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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ысиииъб3
Homo sapiens, clone IMAGE:3162672, mRNA, partial cds.
BC000563
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/clone="IMAGE:3162672"
/tissue_type="Brain, neuroblastoma"
/clone_lib="NH_MGC_19"
                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.nisc.nih.gov/
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                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                           BC000563.1 GI:12653576
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1983)
Pacholczyk,T., Blakely,R.D. and Amara,S.G.
Expression cloning of a cocaine- and antidepressant-sensitive human noradrenaline transporter
Nature 350 (6316), 350-354 (1991)
2008212
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LIAGMPLFYMELALGOYNREGATVWRICPPFRGVGYAVILIALYVGFYNV1 IAWSI
YYLFSSFTLNLPWTDCGHTWNSPNCTDPKLLNGSVLGNHTKYSKYKFTPAABFYERGV
   PRI 07-JAN-1995
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LHURYTLPOKANGINNYTHIPFYRKEATVWIDARDFESLGAGFVULIAPRSYNK
FUNNYTBALLTSSINGINSTRYGFAIFSILGYMAHBHKVNIEDVATEGAGIVFILAPR
ENISTISGSTFWAVVFFVMLLALGELDSSWGGMEAVITGLADDFQVLKRHRKLFTFGVT
STFLLALGTIKGGIYVLTLLDFTFAAGTSILEPAVLMRBIGSWFYGVDDFSRNIQQM
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VLVPIYVIXKFLSTGGSLWERLAYGITPENEHHLVAQNDIROPOLOHMLAI"
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Myers,J.C., Kivirikko,S., Gordon,M.K., Dion,A.S. and Pihlajaniemi,T. Identication of a previously unknown human collagen chain, alpha 1(xV), characterized by extensive interruptions in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMCOLAIXV 2127 bp mRNA linear PRI 27-APR-19 Homo sapiens alpha-1 type XV collagen mRNA sequence. L01697. L01697. I GI:180088 alpha-1 type XV collagen. Homo sapiens (library: gtil from Clonetech Laboratories) placenta con
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HUMNORTR 1983 bp mRNA linear Human noradrenaline transporter mRNA, complete cds.
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100.0%; Pred. No. 6.6e+02;
iive 0; Mismatches 0;
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1. .1983
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/db_xref="taxon:9606"
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                                                                                                                   noradrenaline transporter. Human, cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="Unassigned"
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                                                                                          M65105.1 GI:189257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identification of a previously unknown human collagen chain, alpha 1(XV), characterized by extensive interruptions in the triple-helical region Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10144-10148 (1992) 93066196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primary structure of the alpha 1 chain of human type XV collagen and exon-intron organization in the 3' region of the corresponding
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5161)
Myers,J.C., Kivirikko,S., Gordon,M.K., Dion,A.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-1 type XV collagen.
Homo sapiens (tissue library: Clontech bases 955-5167) umbilical
cord (bases 1-954) cDNA to mRNA.
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Kivirikko,S., Heinamaki,P., Rehn,M., Honkanen,N., Myers,J.C. and
Pihlajaniemi,T.
                                                                                                                                                                                                                                                                                      Gaps
triple-helical region
Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10144-10148 (1992)
33066196
1279671
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HOMO Sapiens alpha-1 type XV collagen mRNA, complete cds.
L25286
                                                                                   1. -2127

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/db_xref="taxon:9606"

/tissue_type="placenta"

/tissue_lib="gt11 from Clonetech Laboratories"

/fissue_lib="gt11 from 392 t
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/tlssue_lib="Clontech bases 955-5167"
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94148920
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/partial
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/citation=[2]
/codon_start=1
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Matches 15; Conservative
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INTPPTPSSPFEDMELSGEPVPEGTLETTNMGIIOHSSPKOGSGEILNDTLEGVHSVD
GDPITDSGSGAGAFLDIAEEKNLAATAAGLAEVPISTAGEAEASSVPTGGPTLSMSTE
NPEECVTPGPDNEERLRATAAGEAEALASMPGEVEASGVAPGELDLSMSAQSLGEEAT
                                                                                                                                                                                                                                       EQGEKGEPGALITEDIPLERLAGKKGEPGAHGAPGPGPKGPPGHKGEFGLJEGFPGFR
GLNGIKGTKGDFGVIMGPPGLPGPFGPPGPPGAVINIKGAIFPIPVRPHCKMPVDTA
HPGSPELITHGVKGEKGSWGLPGSKGEKGDQGAOGPPGPDLAYTHHFLNNIKGEN
GDKGFKGEKGEKGENGINGSFLAGSPGLPGFNPGPAGGNGETVVGPGPPGAPGLPGPP
FGRPGDPGPPGPPGPPAILGAAVALPGPPGPGPGCPGCARVATAFSNNDDMLO
KAHLVIEGTFIYLRDSTEFFIRVRDGWKKLOLGELIPIPADSPPPRALSSNPHOLLPP
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LQQLTVHPDPRTPEELCDPEESSASGETSGLQEADGVAEILEAVITYAASPKEAKVEP
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QLIGDPLPSSVSFVTGYGGFPAXSFGPGANVGRPARTLIPSTFFRDFAIRLVVKPSST
                                                                                                       RGGVLFAITDAFQKVIYLGLRLSGVEDGHQRIILYYTEPGSHVSQEAPAFSVPVMTHR
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Mus musculus clone RP23-117121, LOW-PASS SEQUENCE SAMPLING.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 61956)
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This sequence was identified as CDM:10213135 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This is a 'Working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Mus musculus, clone RP23-117121
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Mus musculus.
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McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C., H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhan, P., Pierre, M., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, V., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viell, R., V., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted MANON-2001) Whitehead Institute/MIT Center for Genome Streat, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu
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55 24254; gap of 100 bp 15 24914; contig of 660 bp in length 16 2504; gap of 100 bp 25 2597; contig of 683 bp in length 18 25797; gap of 100 bp 16 2570; contig of 673 bp in length 16 27328; contig of 673 bp in length 18 27328; contig of 758 bp in length 19 27428; gap of 100 bp 100 
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28864: contig of 647 bp in length
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S Birren, B., Lihton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkly, L., Boderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkly, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, M., Iliev, I., Johnson, R., Landers, S., Landers, T., Lehorczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Monson, L., Mlova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Petta, R., Rieback, M., Riley, R., Santos, R., Schauer, S.,
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 65851)
Birran, B. Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP13-519019
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Homo sapiens chromosome 17 clone RP13-519019 map 17, LOW-PASS SEQUENCE SAMPLING.
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131 43430: gap of 100 bp 44096: contig of 666 bp in length 44096: contig of 666 bp in length 100 bp 44852: contig of 656 bp in length 153 44952: gap of 100 bp 100 
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71: contig of 664 bp in length
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51107: cont
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AC124280.3 GI:22004380
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36124: contig of 748 bp in length

124: gap of 100 bp

36946: contig of 722 bp in length

146: gap of 100 bp

37776: contig of 730 bp in length
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10534: contig of 720 bp
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186: gap of 100 bp
33595: contig of 709 bp
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                                                                                       Ultract Submission
Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 6581)
Barna, N. Bastien, V. Bloom, T. Boguslavkiy, L. Boukhgalter, B., Camarata, J., Charg, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardon, J., Grahmino, K., Diaz, J.S., Dodge, S., Gardon, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., MacLean, C., Macdonald, P., Major, J., Matthews, C., MacLean, C., Macdonald, P., Major, J., Matthews, C., Mordin, J., Wolly, C., Noylor, J., Wolly, C., Novel, C., Norbu, C., Norman, C., Phunkhang, P., Pierre, N., Raymon, C., Nicol, R., Norbu, C., Norman, C., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Travers, M., Vassillev, H., Viel, R., Wilson, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Wollson, B., Stange-Thomann, N., Young, G., Zainoun, J., Viel, R., Wollson, B., Stange-Thomann, N., Young, G., Zainoun, J., Chander, A., and Zody, M., Direct, Bubilsson, B., Stange, F., Markers, M., Vassillev, H., Direct, Submission
Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 30, 2002 this sequence version replaced gi:21699374.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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of 730 bp in length
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f 721 bp in length
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f 722 bp in length
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Web site: http://www-seq.wi.mit.edu
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3166:
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6473:
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7300:
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COMMENT

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Gaps

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AC009031 90280 bp DNA linear HTG 26-JAN-2000
Homo sapiens chromosome 16 clone RP11-13M21, LOW-PASS SEQUENCE
SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 90280)
DioE Joint Genome Institute.
Direct Submisted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA On Jan 26, 2000 this sequence version replaced gi:5686044.
                             /clone_lib="cr-1j6"
/note="This is one of two clone in the same well cr-lj6"
14154 a 25825 c 24793 g 15894 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90280)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This record contains 87 individual
* Sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low Pass Sequence sampling is useful for
identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                           Length 80669;
                                                                                                                                                                                                    Indels
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                                                                                                                                                   Score 15; DB 2; Pred. No. 6.5e+02;
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Unpublished
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Center Code: JGI
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100.0%;
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HTG; HTGS_PHASE0.
HOMO sapiens.
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AC009031/c
LOCUS
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Chlamydomonas reinhardtii clone cr-1j6, WORKING DRAFT SEQUENCE, 1
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Direct Submission
Submitsed (14-ANG-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
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HTGS. PRASE2; HTGS. DRAFT.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 80669)
Wu, H., Lin, S., Jia, H., Dutcher, S. and Roe, B.A.
Chlamydomonas reinhardtii BAC Clone cr-1j6
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              38578 38677: gap of 100 bp 33998: contig of 721 bp in length 39499 40210: contig of 712 bp in length 40211 40310: gap of 100 bp 100 bp 40211 40313: contig of 733 bp in length 40311 41043: contig of 733 bp in length
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38577: contig of 701 bp in length
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/organism="Chlamydomonas reinhardtii"
/db_xref="taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 15; DB 2; I
100.0%; Pred. No. 6.5e+02;
iive 0; Mismatches 0;
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41859: con'
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Matches 15; Conserv
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gap of unknown length
contig of 793 bp in length
gap of unknown length
contig of 652 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 1133 bp in length
gap of unknown length
contig of 1133 bp in length
gap of unknown length
contig of 1079 bp in length
gap of unknown length
contig of 1079 bp in length
gap of unknown length
contig of 1079 bp in length
gap of unknown length

37178:

38597:

39399: 40532: 41611: 42657: 43644: 44808:

36526:

33804: 34775: 35568: gap of contig gap of contig

46147:

47217: 48521: 49309:

	33730	33805	34776		35569	36527	37179	38598	39400	40533	41612	42658	43645	44809	46148	47218	48522	49310	50844	52194	53318	54464	55712	56684	58210	59764	61210	62916	04150	65838	67326	68611	70087	71289	73311	74259	
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9 bp in length	wn length 2 bp in length	unknown length	of 744 bp in length unknown length	of 761 bp in length	wn rengtm 3 bp in length	wn length 9 bp in length	wn length 7 bp in length	wn length 2 bp in length	unknown length of 769 bp in length	wn length 5 bp in length	wn length 2 bp in length	unknown length of 874 bp in length	unknown length of 594 bp in length	nown length 756 bp in length	unknown length of 821 bp in length	wn length 4 bp in length	unknown length of 603 bp in length	wn length 5 bp in length	unknown length of 713 bp in length	wn length 3 bp in length	unknown length of 1215 bp in length	nown length 996 bp in length	unknown length of 623 bp in length	nown length 661 bp in length	unknown length of 625 bp in length	unknown length of 298 bp in length	unknown length of 624 bp in length	nown length 783 bp in length	of 708 bp in length	unknown lengtn of 77 bp in length	nown length 866 bp in length	nown length 918 bp in length	nown length 766 bp in length	wn length 1 bp in length	unknown length of 702 bp in length	wn length 46 bp in length	wn Length 11 bp in length
contig of 689					ap of unkilo ontig of 74	gap of unkno contig of 65	ap of unkno ontig of 74	gap of unkno contig of 83	ap of unkno ontig of 76	gap of unkno contig of 65	ap of unkno ontig of 80	gap of unkno contig of 87	gap of unkno contig of 59		gap of unknown contig of 821 b	gap of unkno contig of 64	ap of unkno ontig of 60	gap of unkno contig of 62	gap of unkno contig of 71	ip of unkno	np of unkno	gap of unkno contig of 99	unk of		gap of unknown contig of 625 k				contig of 70		of	or unk ig of	gap or unknown contig of 766 k	-			gap or unknown contig of 1211
6962: C	9. 7734: C			9239: 🤆	9982: cc	97 10641: CC	94 11388: C	96 12220: CC	97 12989: CC	g; 13644: CC	gë 14446: CC	98 15320: CC	97 15914: CC	16670: cc		g: 18135: CC						ge 23060: cc	98 23683: CC	98 24344: CC	ge 24969: cc	95 25267: cc	25891: CC	26674: CC	27382: cc	27459: cc	98 28325: CC	g8 29243: CC	30009: CC	95 30770: CC	98 31472: CC	98 32518: CC	98 33729: cc
6274	6963	0 0	7735	8479	9240	6863	10642	11389	12221	12990	13645	14447	15321	15915	16671	17492	18136	18739	19364	20077	.20850	22065	23061	23684	24345	24970	25268	25892	26675	27383	27460	28326	29244	30010	30771	31473	32519
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gap of unknown length contig of 1350 bp in length gap of unknown length contig of 1124 bp in length aap of unknown length of 1164 bp in length of 1839 bp in length of unknown length in length of unknown length length of 1870 bp in length of unknown length of unknown length of 188 bp in length of unknown length of unknown length of unknown length of 1834 bp in length of 1885 bp in length of unknown length g of 1146 bp in length f unknown length g of 1248 bp in length f unknown length g of 972 bp in length f unknown length g of 1202 bp in length if unknown length g of 2022 bp in length f unknown length g of 948 bp in length f unknown length g of 1578 bp in length f unknown length length bp in length length bp in length length of 1526 bp in length unknown length of 1534 bp in length unknown length bp in length bp in length length bp in length length bp in length length bp in length bp in length length unknown gap of contig contig gap of 54463: 55711: 65998: 56683: 50843: 52193: 53317: 58209: 59763: 62915: 64134: 67325: 68610: 70086: 71288: 73310: 74258: 75836: 61209:

Length 90280;

DB 2;

Score 15;

100.08;

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Peery, J., Percezi, Oragunye, N., Oviedo, R., Pace, A., Payton, B., Ouiles, M., Percezi, D., Peters, L., Pickens, R., Primus, E., Pu.L. L., Ouiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Ponce, M., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Stutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, P., Tamerisa, R., Tanerisa, K., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Warten, Wall, R., Wang, S., Warten, W., Wall, R., Wang, S., Warten, W., Wallstams, G., Walliams, G., Walliams, G., Walliamson, A., Wleczyk, R., Wooden, S., Weinstock, G. and Gibbs, R., Stou, J., Zorrilla, S., Nelson, D., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                      Vorley, K.C.
Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TY 77030, USA
On Dec 20, 2001 this sequence version replaced g1:15624602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 65 contigs. The true order of the piaces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* truns of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consensus quality: 115371 bases at least 040 Consensus quality: 123148 bases at least 030 Consensus quality: 129020 bases at least 020 Estimated insert size: 114258; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose fp estimation Quality coverage: 1.6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7731: contig of 7731 bp in length 7831: gap of unknown length 12932: contig of 5101 bp in length 13032: gap of unknown length 19264: contig of 6232 bp in length 19364: gap of unknown length 24766: contig of 5402 bp in length 24866: gap of unknown length 24866: gap of unknown length 24866: gap of unknown length 24861: contig of 4415 bp in length 29281: contig of 4415 bp in length
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LAFLCHR12_5 500001 610000
LAFLCHR12_6 600001 710000
LAFLCHR12_7 700001 757191
Continuation (2 of 8) of LAFLCHR12 from base 100001 (AL390114 Leishmania major chromosom
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16075)
Chu,T., Blumenfeld,M. and Cohen,D.
Biallell: markers derived from genomic regions carrying genes involved in central nervous system disorders
Patent: WO 0151659-A 544 19-JUL-2001;
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/note="99-32148-315.mis complement"

31844. 31862

34799. 334930
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Pred. No. 6.5e+02;
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21207. .21387
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31535. .31559
/note="99-32148-315.probe"
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/note="exon 4"
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37172. 37409
/note="exon 3"
50215. 50233
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primer_bind

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$0558

$0559. .5057

**Note="19-51-347: polymorphic base A or G"

$0559. .5057

**Note="19-51-347.mis complement"

$0513. .50513. polymorphic base A or G"

$0559. .5057

**Note="19-51.rp complement"

$05261. .57395

**Note="exon 5"

$0355. .59458

**Note="exon 5"

$0559. .50747

**Note="exon 7"

$05050. .5018

**Note="19-56.pu"

$0311. .63150

**Note="19-56.pu"

$0321. .6328

**Note="19-56-140.mis"

$0328. .6328

**Note="19-56-140.mis"
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/0211. 183289

/note="19-56-140: polymorphic base A or G"

/note="19-56-140.mis complement"

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/note="19-56.rp complement"

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/note="19-44-251.mis"

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/note="19-44.rp complement" 65187. 65654
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67671. 67928

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December 11, 2002, 12:23:57; Search time 212.5 Seconds (without alignments) 158.965 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2185239 seqs, 1125999159 residues
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Maximum Match 1008
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result	Score	% Query Match	% Query Match Length DB	DB	ID	Description
1	15	100.0	15	22	!	Probe for human no
2	15	100.0		23	AAH88259	CNS disorder-relat
Э	15	100.0	920	23	AAH88264	CNS disorder-relat
4	15	100.0		22	AAH28088	Nucleotide sequenc
c 5	15	100.0	1044	23	AAS80746	DNA encoding novel
9	15	100.0		22	AAH28082	Nucleotide sequenc
7	15	100.0		22	AAH28086	Nucleotide sequenc
œ	15	100.0		13	AAQ28118	Human norepinepher
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                                                                        a human norepinephrine transporter gene. The specification a method for screening for susceptibility to sub-optimal norepinephrine transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the susceptibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter genes are useful for gene therapy for modulating norepinephrine transport in a target cell and treating susceptibility.
                                                                                                                                                                                                                                                        to impaired norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single nucleotide polymorphism; SNP; biallelic marker; human; ds; central nervous system disorder; CNS; NET; norepinephrine transporter.
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particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
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                                              Claim 15; Page 69; 133pp; English.
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Best Local Similarity
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The present invention relates to biallelic markers derived from human

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genes involved in central nervous system (CNS) disorders. The present sequence is one such biallelic marker derived from human norepinephrine transporter (NET) gene. This marker has a single nucleotide polymorphism (SNP) and is useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set of genetic markers in a biological sample, where the markers comprise at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to biallelic markers derived from human genes involved in central nervous system (CNS) disorders. The present sequence is one such biallelic marker derived from human norepinephrine transporter (NET) gene. This marker has a single nucleotide polymorphism (SNP) and is useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single nucleotide polymorphism; SNP; biallelic marker; human; ds; central nervous system disorder; CNS; NET; norepinephrine transporter.
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                                                                                                          least one CNS disorder related marker.
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Best Local Similarity
Matches 15; Conserv
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misc_feature
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                                                                                                                                                                                                                                                                          mental illness; hypertension; heart disease; stimulant abuse; cocaine; amphetamine abuse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene
                                                                                                                                                                                                                        Nucleotide sequence of a exon 9 of norepinephrine transporter gene.
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                                                                                                                                                                                                                                                          Norepinephrine transporter; orthostatic intolerance; gene therapy,
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                 170 CCTTCTCGCCCTGTT 184
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical immaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymorleotide sequences have applications in
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #16550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 16550; 103pp; English.
                                                                                                                                                                                              )746/c
AAS80746 standard; cDNA; 1044 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
230 CCTTCTCGCCCTGTT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639362/73
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les 15; Conserv
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                                                                                                                                                                                          AAS80746/
                                                                                                                                                       RESULT 5
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Best Local Similarity 100. Matches 15; Conservative

Query Match

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Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene
                                                                                                                                                 Nucleotide sequence of a human norepinephrine transporter.
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                      AAH28086 standard; DNA; 1854 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-1999; 99US-0173682.
11-JAN-2000; 2000US-0175456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-2000; 2000WO-US35491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYVA-) UNIV VANDERBILT
                                                                                                                                                                                                                                 amphetamine abuse; ss.
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P-PSDB; AAB84534.
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                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                          05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2001
                                                                  AAH28086;
                                                                                                                                                                                                                                                                                                              Key
                                                              The present sequence encodes a human norepinephrine transporter. The specification a method for screening for susceptibility to sub-optimal norepinephrine (NE) transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the subsectibility of the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter genes are useful for gene therapy for modulating norepinephrine transport in a target cell and treating susceptibility to impaired norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, hypertension, heart disease, psycho
                                                                                                                                                                                                                                                              Norepinephrine transporter; orthostatic intolerance; gene therapy; mental illness; hypertension; heart disease; stimulant abuse; cocaine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for susceptibility to sub-optimal norepinephrine transport, particularly orthostatic intolerance in a subject by detecting a polymorphism of norepinephrine transporter gene .
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                                                                                                                                                                                                                        Nucleotide sequence of a human norepinephrine transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "norepinephrine transporter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1854 BP; 356 A; 554 C; 494 G; 450 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 75; Page 98-101; 133pp; English
                                                                                                                                                                                                                                                                                                                                                                                   Socation/Qualifiers
                                                                                                  AAH28082 standard; DNA; 1854 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-DEC-2000; 2000WO-US35491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-1999; 99US-0173682.
11-JAN-2000; 2000US-0175456.
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blakely RD;
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97 CCITCICCCCTGIT 83
                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                        amphetamine abuse; ss.
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                         AAH28082;
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                                                            RESULT 6
                                                                                 AAH28082
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A PART OF THE PROPERTY OF THE

Blakely RD;

/product= "norepinephrine transporter"

Location/Qualifiers 1..1854 /*tag= a

(first entry)

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                                                                                                                                                                                                                                                                                      for gene therapy for modulating norepinephrine transport in a target cell and treating susceptibility to impaired norepinephrine transporter function, orthostatic intolerance or other relevant diseases in humans and animals such as mental illness, hypertension, heart disease, psychostimulant abuse e.g. cocaine or amphetamine abuse.
The present sequence encodes a human norepinephrine transporter. The specification a method for screening for susceptibility to sub-optimal norepinephrine (NB) transport in a subject. The method comprises obtaining a biological sample from the subject and detecting a polymorphism of a norepinephrine transporter gene in the sample from the subject, the presence of the polymorphism indicating the subject to sub-optimal norepinephrine transport. The method is useful for screening for susceptibility of a subject to orthostatic intolerance. Norepinephrine transporter genes are useful
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Best Local Similarity 100.
Matches 15; Conservative
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AAQ28118
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1362 CCTTCTCGCCCTGTT 1376

RESULT 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                   NT; noradrenaline; neuroblastoma; neutotransmitter; antidepressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementary DNA clone encoding human norepinephrine transporter protein - isolated from human neuroblastoma cells and useful for determining action of e.g. antidepressant drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              name cell. Such studies include the relative effects of various psychotropic) drugs such as antidepressants.
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                                               Human norepinepherine transporter protein cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                    Location/Qualifiers
61..1914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 1; 37pp; English.
                                                                                                                                                                                                                                                                                                           92WO-US01376.
                                                                                                                                                                                                                                                                                                                                           91US-0676980.
               15-MAR-1993 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-366242/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAR26416.
                                                                                                                                                                                                                                                                                                           20-FEB-1992;
                                                                                                                                                                                                                                                                                                                                           28-MAR-1991;
                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                      WO9217568-A
                                                                                                                                                                                                                                                                       15-0CT-1992
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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level in an unactivated at expression level in an unactivated activation level to an expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting GCA with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the cubject to a pathogen or sterile inflammatory disease, by detecting the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the cubject to a pathogen or sterile inflammatory disease, by detecting the cubject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. MI is useful for detecting an agent capable of modulating corresponse in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, (e.g. psoriasis, rheumatoid arthitis, and and inflammation injury, ARDS, adult respiratory distress syndrome, response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, (e.g. psoriasis, rheumatoid arthitis, periodontal disease, also bacterial infection, viral infection, contining the proposition of the paralled infection of the paralled of paralled or periodontal disease, also bacterial infection and MS is the paralled or the paralled or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part form the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                               Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohm's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                    Human cDNA differentially expressed in granulocytic cells #433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vockley J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weissman SM, Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-OCT-2001; 2001WO-US30821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2000; 2000US-237189P
14-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-435328/46.
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                                                                                                                                                                                                                                                                                                                                                                                 WO200228999-A2
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                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes involved in central nervous system (CNS) disorders (see MARBARG-AAHB8RO). The markers have a single nucleotide polymorphism (SNP) and are useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set of genetic markers in a biological sample, where the markers comprise at least one CNS disorder related marker. The present sequence was used to illustrate the invention.
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to biallelic markers derived from human
                                                                                                                                                                                                                                                                                                                                                                                               Isolated polynucleotides, useful for genotyping nucleic acids for biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 160755 BP; 43057 A; 36601 C; 38189 G; 42727 T; 181 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 160755;
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0
                    Length 5161;
                                                                                                                                                                                                         Single nucleotide polymorphism; SNP; biallelic marker; human;
Sequence 5161 BP; 1254 A; 1420 C; 1363 G; 1124 T; 0 other;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                  ch 100.0%; Score 15; DB 24; Similarity 100.0%; Pred, No. 1.9e+02; 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 15; DB 23; 100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                   central nervous system disorder; CNS; ds
                                                                                                                           AAH88704 standard; DNA; 160755 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN18096 standard; cDNA; 336 BP.
                                                                                                                                                                                                                                                                                                                                                            Cohen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                       Human DNA sequence SEQ ID 544,
                                                                                                                                                                                                                                                                                                11-JAN-2001; 2001WO-IB00116.
                                                                                                                                                                                                                                                                                                                     13-JAN-2000; 2000US-0175854
                                                                                                                                                                 26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 63345 CCTTCTCGCCCTGTT 63359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                   2673 CCTTCTCGCCCTGTT 2659
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                                                        1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                          Chu T, Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCTTCTCGCCCTGTT
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483085/52.
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Best Local Similarity
Matches 15; Conserv
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                         WO200151659-A2
                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 - JUN - 2002
                                                                                                                                                                                                                                                                            19-JUL-2001
                                                                                                                                                AAH88704;
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                                      Matches
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                                                                                                                  AAH88704
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                                                                                                                                                                                            cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human polypeptides and polynucleotides useful for diagnosing,
                                                                    Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage degenerative disorder; osteoarthritis; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 336 BP; 61 A; 101 C; 109 G; 64 T; 1 other;
Human ORFX polynucleotide sequence SEQ ID NO:4669.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID 4669; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                    myasthenia gravis; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-106308/14.
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Les 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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Ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; infinammatory condition; immune disorder; blood disorder;
                                                                                                                                                                      cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                            ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                    Human ovarian antigen HVVAW26 cDNA, SEQ ID NO:2083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 2083; 2922pp; English.
           ABQ56203 standard; cDNA; 655 BP.
                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                              07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                                                                                       07-JUN-2001; 2001WO-US18569.
                                                            22-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                Birse CE, Rosen CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ABP43126
                                                                                                                                                                                                                                                                      WO200200677-A1.
                                                                                                                                                                                                                                                Homo sapiens.
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                                   ABQ56203;
ABQ56203/c
ID ABQ56
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDMAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 90% identical to the sequences of the invention. The invention additionally relates to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies and polypeptides in diagnosing of ovarian antigen polynucleotides and polypeptides in diagnosing. Irrating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system castatic ovary syndrome, ovarian cysts, and dysmenorihoea, endocrine disorders (e.g., infertility, disorders of pregnancy, anovulation.

Cliscoters, infections (e.g., chlampida, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), but all and acquired independence (e.g., chlampida, HIV) toxoplasmosis, and confidence immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), but all and acquired insorders (e.g., congenital and acquired blood-related disorders (e.g., anaemia), cardiovascular disorders, (e.g., anaemia), cardiovascular disorders), and encorders (e.g., anaemia), cardiovascular disorders, encorders (e.g., anaemia), cardiovascular disorders, autoimmune disorders (e.g., anaemia), cardiovascular disorders, autoimmune disorders (e.g., anaemia), cardiovascular disorders, autoimmune disorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardio
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Note: The sequence data for this patent did not form part of the printed

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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                                                                                  Length 655;
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                                                                                                                  Indels
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                                                 12 other;
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                                                                                                Pred. No. 5.8e+02;
Mismatches 0;
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                                                                                  DB 24;
                                                Sequence 655 BP; 182 A; 168 C; 177 G; 116 T;
                                                                    93.3%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                   BP.
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2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                 organic acid synthesis; ds
                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                2 CTTCTCGCCCTGTT 15
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                                                                                                                                                                 556 CTTCTCGCCCTGTT
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03-AUG-2000;
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Tateishi N,
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                                                                                  Query Match
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The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID NO 29951.
                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
                                                                                                     ABL11823 standard; cDNA; 2036 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               PWD,
                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                     pharmaceutical; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
            250 CCTTCTCGCCCTGT 237
                                                                                                                                                                                                                                                                   Drosophila melanogaster
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CCTTCTCGCCCTGT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interactions -
                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                                                                                                                            27-SEP-2001.
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                                                                                                                                 ABL11823;
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                                                                        RESULT 14
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                                                                                      ABL11823,
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ID AAQ1
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specification.
The 20.5 gene, also referred to as Tea, identifies transcripts found in only a limited number of tissues. Tea transcripts are induced in splenocytes activated with the T cell mitogen ConA. Unlike other known genes expressed in activated T cells, the Tea gene appears to encode a protein which traverses the membrane multiple times, whereas the large number of known integral membrane protein which are induced in T cell activation are single membrane spanning proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                             used to
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                                      Multiple membrane spanning protein; T cell; development; ss.
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                                                                                                                                                                                                                                                                                                                                                         New recombinant polypeptide comprising a T-cell protein regulate T-cell development and tumorigenic phenotype and block T-cell activation in auto:immune disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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ches 0;
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Job time: 241.5 secs
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                                                                                            Location/Qualifiers
410..1767
/*tag= a
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                                                                                                                                                                                                                                                              (REDE-) RES DEV FOUND
            Tea gene (cDNA 20.5).
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                                                                                                                                                                                                                                                                                                                 WPI; 1991-339818/46.
P-PSDB; AAR14645.
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Best Local Similarity
Matches 14; Conserv
                                                                    Mus musculus
                                                                                                                                                                                                         12-APR-1990;
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                                                                                                                                                                              31-OCT-1991
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Scoring table:

Searched:

Database

Perfect score:

Sequence:

OM nucleic

Run on:

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Sequence 6, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 76, Appli
Sequence 1, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 37, Appl
                                                                                                                                                                                                                                                                                      Sequence 108, App
Sequence 1, Appli
Sequence 12, Appl
Sequence 18, Appl
Sequence 20, Appl
                                               Sequence Sequence Sequence
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                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/07686322A
Patent No. 5312733
GENERAL INFORMATION:
APPLICANT: MacLeod Dr., Carol L.
TITLE OF INVENTION: No. 5312733el T-cell Lymphoma cDNA Clones
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Department, Fulbright & Jaworski
STREET: 1301 McKinney, Suit 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1301 MCKinney, Suit 5100
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77010-3095
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                   US-09-491-522-6
US-09-491-522-2
US-09-171-337A-4
US-08-261-206A-76
US-09-254-325-1
                                                                                                                                                                                      US-09-491-522-1
US-08-306-691B-19
PCT-US93-06251-19
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US-08-094-079-18
US-08-094-079-20
US-08-094-079-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Launer, Charlene A.
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: D-5232-CIP
TELECOMMINICATION INFORMATION:
TELEFAX: (713) 651-5246
TELETAX: (713) 651-5246
TELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/686,322A
FILING DATE: 19910411
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/509684
FILING DATE: 13-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SL12 cell line
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INDIVIDUAL ISOLATE: SL12 cell
TISSUE TYPE: Lymphoma
CELL TYPE: T-cell
CELL LINE: SL12.3 and SL12.4
IMMEDIATE SOURCE:
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  Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 137, App
Sequence 137, App
Sequence 29, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 24, Appl
Sequence 24, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 1, Appli
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Sequence 3, Appli
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                                                                                                                                                                                         (without alignments)
97.876 Million cell updates/sec
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Sequence 1,
Sequence 22,
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                                                                                                                                                             December 11, 2002, 13:29:32; Search time 47 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: /cgg_2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                      GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-961-527-320
US-08-50-766-2
US-08-50-766-2
US-08-379-496-1
US-08-650-766-3
US-08-650-766-3
US-08-650-766-1
US-08-650-766-1
US-08-650-766-1
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PCT-US95-10398-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-927-597-29
US-09-605-785-747
US-09-105-537-9
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PCT-US92-09382-5
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US-09-103-840A-1
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US-08-927-597-29
                                                                                                                                                                                                                                                                                                                                                                                                                             441362 seqs, 153338381 residues
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                                                                                                                   - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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10322
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Match Length
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89.3
89.3
86.3
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Score

Result Š.

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APPLICANT: MERUELO, DANIEL
APPLICANT: YOSHIMOTO, TAKAYUKI
TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: FLORPY disk
COMPUTER: IBM PC compatible
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/132,990A
FILING DATE: 09.0404,729
FILING DATE: 29.JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05569
FILING DATE: 11.JUN-1993
PRIOR APPLICATION NUMBER: 07/899,075
FILING DATE: 11.JUN-1992
PRIOR APPLICATION NUMBER: 07/899,075
FILING DATE: 11.JUN-1992
PRIOR APPLICATION NUMBER: 07/806,178
FILING DATE: 11.JUN-1992
PRIOR APPLICATION NUMBER: 07/806,178
FILING DATE: 11.DUN-1991
PRIOR APPLICATION NUMBER: 07/806,178
FILING DATE: 14.DEC-1991
PRIOR APPLICATION NUMBER: 07/627,950
FILING DATE: 14.DEC-1990
ATTORNEY, AGENCEY, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application PC/TUS9209382 ; GENERAL INFORMATION:
                                                                               Sequence 5, Application US/08132990A; Patent No. 5834589; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 790-9090
TELEFAX: (212) 669-8864
TELEA: 6641 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2397 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 93.3
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 1379 CTTCTCGCCCTGTT 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410..1768
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                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
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US-08-132-990A-5
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PCT-US92-09382-5
                                                    US-08-132-990A-5
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                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08002999
Patent No. 5440017
GENERAL INFORMATION:
GENERAL INFORMATION:
MACLEOD DI., Carol L.
TITLE OF INVENTION: No. 5440017el T-cell Lymphoma cDNA Clones NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Department, Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                  DB 1; Length 2397;
84;
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                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUW TYPE: FI-DPPP disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,999
FILING APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/686,322
FILING APPLICATION NUMBER: US 07/686,322
FILING APPLICATION NUMBER: US 07/686,322
FILING APPLICATION NUMBER: US 07/686,322
FILING ADDITION NUMBER: US 07/686,322
FILEFRATION NUMBER: US 07/686,322
FILEFRATION NUMBER: US 07/686,322
FILEFRATION NUMBER: US 07/686
FILEFRAX: (713) 651-5587
TELEFRAX: (713) 651-5587
                                                             93.3%; Scot. 100.0%; Pred. No. c... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Preu. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
                                                                            Query Match 93.3
Best Local Similarity 100.
Matches 14; Conservative
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INDIVIDUAL ISOLATE: SI
TISSUE TYPE: Lymphoma
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                              Db 1379 CTTCTCGCCCTGTT 1392
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                                                                                                                                                                                              2 CTTCTCGCCCTGTT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 77010-3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: 20.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Texas
; CLONE: 2
US-07-686-322A-5
                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-08-002-999-5
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STATE:
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Sequence 137, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF SISCLATES OF HEBPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DEALVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.4; DB 2; Length 573; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.6e
; Mismatches
                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
ыск: US/08/290,665A
15-AUG-1994
18-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC COMPATIBLE SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: MORGAN & FINNEGAN
345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 573 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: S2
US-08-290-665A-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MUCITITE OF INVENTION: AMINITIEE OF INVENTION: CORE TITLE OF INVENTION: AND HITLE OF INVENTION: SEQUENCES: 263 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531 CCTTCTTGCCCTGTT 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: NEW YORK STATE: NEW YORK
                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
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STREET: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                          APPLICANT: YOSHIMOTO, TAKAYUKI
ITILE OF INVENTION: Human Retrovirus Receptor and DNA Coding
ITILE OF INVENTION: Therefor
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Patent No. 582852
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NOCLEOTIDE AND DEDUCED
TITLE OF INVENTION: CORE GENES OF ISOLATES OF
TITLE OF INVENTION: CORE GENES OF ISOLATES OF
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC MENUMENT OF SEQUENCES IN DIAGNOSTI
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                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19921213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MERUELO-1
                                                                                                                                                                                         E: Browdy and Neimark
419 Seventh Street, N.W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Livrat. Shmuel
REGISTRATION NUMBER: 33,949
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFHONE: 202 628-5197
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2397 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MORGAN & FINNEGAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
               MERUELO, DANIEL
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CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 14; Conservative
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ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
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410..1768
                                                                                                                                                          CORRESPONDENCE ADDRESS:
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TYPE: NUCLEIC ACID
STRANDEDNESS: singl
                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                               Arens 415
STREET: 415
TTY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-08-290-665A-137
                                                                                                                                                                                                                                                                                                                                    20004
                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION:
PCT-US92-09382-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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                                                                                                                                                                                                                                                                                                         COUNTRY:
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Gaps

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APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUXSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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       Length 630;
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
     89.3%; Score 13.4; DB 3;
93.3%; Pred. No. 1.6e+02;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PROR APPLICATION DATA:
PROR APPLICATION NUMBER:
FILING DATE: 11-WAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEFANCE: (703) 816-4100
TELEFAX: (703) 816-4100
                                                                                                                                                                        RESULT 8
US-08-927-597-29
; Sequence 29, Application US/08927597
patent No. 6.445503
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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; LOCATION: 1..624
US-08-927-597-29
                                                                                                   177 CCTTCTCGCTCTGTT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 CCTTCTCGCTCTGTT 191
                                                                                1 CCTTCTCGCCCTGTT 15
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..627
                       Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                     g
                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
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                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BUSETENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BOSMAN, FONS
APPLICANT: BUSE, MARIET-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 1111
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUMPRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: U.S/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                            Score 13.4; DB 5;
Pred. No. 1.6e+02;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1487-10
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/08612973 Patent No. 6150134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTATION UNDRER: 32,205
REFERENCE/DOCKET UNDRER: 1487-
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                            89.3%;
TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 base pairs
TYPE: nucleic acid
                                                                                                                                                  ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S2
PCT-US95-10398-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                          Query Match 89.3
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                          531 CCTTCTTGCCCTGTT 545
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                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                       1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE:
                                                                                                                 linear
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                                                                                                               TOPOLOGY: lin
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
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US-08-612-973-29
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GENERAL INFORMATION:
APPLICANT: Charles Kunsch
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STRATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó;
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TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.4; DB 4; Length 1475;
Pred. No. 1.7e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: CIP OF 09/141,908 EARLIER FILING DATE: 1998-08-28 EARLIER APPLICATION NUMBER: CIP OF 09/073,538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTATION NUMBER: 36,33333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/09320878A Patent No. 6117659
                                                                                                                                             Sequence 320, Application US/08961527 Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PB3A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 320:
SEQUENCE CHARACTERISTICS:
LENGTH: 1475 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.3%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: ASHLEY, GATY
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, MATY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 89.3
Best Local Similarity 93.3
Matches 14; Conservative
                       246 CCTCCTCGCCCTGTT 260
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STRANDEDNESS: double
  1 CCTTCTCGCCCTGTT 15
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MEDIUM TYPE: Diskett
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US-08-961-527-320/c
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US-08-961-527-320
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US-09-320-878-24
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hepler, William TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF, PROSTATE CANCER FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 747
LENGTH: 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 738;
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US-09-105-537-9
Sequence 9, Application US/09105537A
Patent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
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93.3%; Pred. No. 1.6e+02;
live 0; Mismatches 1;
                                    Sequence 747, Application US/09605785
Patent No. 6321716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATION: (1)...(738)
; CTHEN INFORMATION: n=A,T,C or G
US-09-605-785-747
                                                                                                 APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
                                                                                                                                                                                      Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                   Fanger, Gary R.
Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 93.3
Watches 14; Conservative
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                                                                                                                                                                                                                                                                                        Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469 CCTTCTCCCCTGTT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                       Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 Li, Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                              GENERAL INFORMATION:
RESULT 9
US-09-605-785-747/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 9
LENGTH: 1458
                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
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6

Gaps

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APPLICANT: MORRISON, Nigel A
APPLICANT: BISAN, John A
APPLICANT: EISMAN, John A
APPLICANT: KELLY, Paul J
TITLE OF INVENTION: Assessment of Trans-Acting Factors Allelic
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                Length 1954;
                                                                                                                                                                                                              Score 13.4; DB 3;
Pred. No. 1.7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Rothwell, Figg, Ernst & Kurz STREET: Suite 701-E, 555 13th Street.N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: December 11, 2002, 15:30:43 Job time: 52 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,496
FILING DATE: 02-MAR-1995
EARLIER APPLICATION NUMBER: 60/012,600 EARLIER FILING DATE: 1996-03-01 NUMBER OF SEQ ID NOS: 22 SOFTWARE: PALENTIN VEr. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1871-114
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08379496 Patent No. 5593833 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 02-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BAIDAIR G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                  89.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.3%;
93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2169 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 89.3
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                  Query Match 89.3
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 CCTTCTCTCCCTGTT 150
                                                                                                                                                                                                                                                                                                                             679 CCTCCTCGCCCTGTT 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                     1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-08-379-496-1/c
                                                                                                            LENGTH: 1954
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                         US-08-922-635-2
                                                                                                                                                                                                                                                                                                                                        PP
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US-08-922-635-2/C

US-08-922-635-2/C

Sequence 2, Application US/08922635A

Patent No. 6033871

APPLICANT: PILETZ, John E.

APPLICANT: IVANOV, Tina R.

TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES

TITLE OF INVENTION: AND POLYPEPTIDES ENCODED THEREBY

FILE REFERENCE: Corrected Sequence Listing

Patent No. 6033871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICAMY: PILETZ, John E.
APPLICAMY: PILETZ, John E.
APPLICAMY: PILETZ, John E.
TYPLE OF INVENTION: METHOD FOR CLONING A HUMAN IMIDAZOLINE RECEPTOR AND TITLE OF INVENTION: METHOD FOR CLONING THE SAME FILLE REFRENCE: COFFECTED Sequence Listing Patent No. 6015690 CURRENT APPLICATION NUMBER: US/08/650,7660 CURRENT PILING DATE: 1996-05-20 EARLIER APPLICATION NUMBER: US 60/012,600 EARLIER FILING DATE: 1996-03-01 SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                  Score 13.4; DB 3; Length 1
Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                     EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1998-02-22
EARLIER FILING DATE: 1998-09-22
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 24
LENGTH: 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/08/922,635A CURRENT FILING DATE: 1997-09-03
EARLIER APPLICATION NUMBER: 08/650,766
EARLIER FILING DATE: 1996-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08650766D Patent No. 6015690
                                                                                                                                                                                                                                                                                            ) ORGANISM: Streptomyces venezuelae US-09-320-878-24
        EARLIER FILING DATE: 1998-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.3%;
93.3%;
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Best Local Similarity 93.3%;
Matches 14; Conservative
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US-08-650-766-2
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Matches 14; Conserv
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US-08-650-766-2/c
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December 11, 2002, 14:35:52; Search time 52.5 Seconds (without alignments) 111.409 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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15
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Published_Applications_NA:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. r. cgn2_6/ptodateA/2/pubpna/USO7_PUBCOMB.seq:*

/ cgn2_6/ptodateA/2/pubpna/USO6_NEW_PUB.seq:*

/ cgn2_6/ptodateA/2/pubpna/USO6_NEW_PUB.seq:*

/ cgn2_6/ptodateA/2/pubpna/USO6_NEW_PUB.seq:*

/ cgn2_6/ptodateA/2/pubpna/USO6_NEW_PUB.seq:*

/ cgn2_6/ptodateA/2/pubpna/USO8_NEW_PUB.seq:*

/ cgn2_6/ptodateA/2/pubpna/USO8_NEW_PUB.seq:*

/ cgn2_6/ptodateA/2/pubpna/USO8_NEW_PUB.seq:*

// cgn2_6/ptodateA/2/pubpna/USO8_NEW_PUB.seq:*

// cgn2_6/ptodateA/2/pubpna/USO8_PUBCOMB.seq:*

// cgn2_6/ptodateA/2/pubpna/USO8_NEW_PUB.seq:*

SUMMARIES

Sequence 26040, A Sequence 13413, A Sequence 15909, A Sequence 12426, A Sequence 747, App Sequence 747, App Sequence 9, Appli Sequence 0, Appli Sequence 1, Appli Sequence 3, Appli Sequence 1, Appli Sequence 3, Appli Sequence 1, Appli Appli Sequence 1, Appli Appli Sequence 1, Appli Description US-09-764-869-2353 US-09-801-874-3 US-09-860-846-3 10 DB Query Match Length 13613 13613 15016 15857 42450 Result Š. υ

3 86.7 3992 10 US-09-944-807-9 Sequence	3 86.7 4558 10 US-09-764-878-258 Sequence	3 86.7 4558 10 US-09-764-860-937 Sequence 937, P	4 82.7 138 10 US-09-783-590-6989 Sequence	4 82.7 148 10 US-09-878-574-14438 Sequence 14438,	4 82.7 173 10 US-09-974-300-7193 Sequence	82.7 258 10 US-09-878-574-6987 Sequence 6987,	4 82.7 262 10 US-09-923-876-3974 Sequence 3974,	82.7 269 10 US-09-878-574-15063 Sequence 15063,	82.7 337 10 US-09-983-965-906 Sequence	4 82.7 356 10 US-09-983-965-5128 Sequence 5128	4 82.7 357 10 US-09-777-564-881 Sequence 881, P	4 82.7 360 10 US-09-777-564-1626 Sequence 1626,	4 82.7 368 10 US-09-777-564-553 Sequence	4 82.7 389 10 US-09-954-456-1577 Sequence 1577,	4 82.7 389 10 US-09-880-107-3234 Sequence	4 82.7 390 10 US-09-960-352-14333 Sequence	4 82.7 413 10 US-09-983-965-968 Sequence	4 82.7 427 10 US-09-983-965-928 Sequence 928,	4 82.7 447 10 US-09-784-423-17 Sequence 17, 1	4 82.7 453 10 US-09-983-965-723 Sequence	456 10 US-09-770-444-528 Sequence 528,	4 82.7 461 9 US-09-954-531-813 Sequence 813, P	4 82.7 467 10 US-09-867-701-10365 Sequence	4 82.7 47	.7 477 10 US-09-969-708-28 Sequence	ALIGNMENTS		US-09-864-761-26040/c ; Sequence 26040, Application US/09864761		Penn, Sharron G.	: Rank, David R. אסיים האיים א	
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D	S-09-864-761-26040/c
••	; Sequence 26040, Application US/09864761
••	Patent No. US20020048763A1
•••	GENERAL INFORMATION:
••	APPLICANT: Penn, Sharron G.
••	APPLICANT: Rank, David R.
••	APPLICANT: Hanzel, David K.
••	APPLICANT: Chen, Wensheng
••	OF INVENTION: H
••	TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICRO
••	FILE REFERENCE: Aeomica-X-1
••	CURRENT APPLICATION NUMBER: US/09/864,761
••	CURRENT FILING DATE: 2001-05-23
••	PRIOR APPLICATION NUMBER: US 60/180,312
••	FILING DATE: 2000-02-04
••	z
••	PRIOR FILING DATE: 2000-05-26
••	PRIOR APPLICATION NUMBER: US 09/632,366
••	PRIOR FILING DATE: 2000-08-03
••	PRIOR APPLICATION NUMBER; GB 24263.6
••	PRIOR FILING DATE: 2000-10-04
••	APPLICATION N
••	FILING DATE:
••	- 1
••	FILING DATE:
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••	FILING DATE:
••	APPLICATION N
••	FILING DATE:
••	PRIOR APPLICATION NUMBER: PCT/US01/00669
•	FILING DATE:
••	Z
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••	APPLICATION N
••	: 2001-01
••	APPLICATION NUMBER:
••	
••	APPLICATION N
••	PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661 PRIOR FILING DATE: 2001-01-30

US-09-861-289-3 US-09-880-107-3783 US-09-764-864-1704 US-09-815-048-3

ARRAY

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APPLICANT: Penh, Sharron G.
APPLICANT: Penh, Sharron G.
APPLICANT: Penh, Sharron G.
APPLICANT: Rak, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US 00/180, 312
PRIOR APPLICATION NUMBER: US 00/207, 456
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 09/632, 366
PRIOR APPLICATION NUMBER: US 09/632, 366
PRIOR PELING DATE: 2000-09-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-07
PRIOR PLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 00/236, 359
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-01-01
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CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1

CTHER INFORMATION: NT HIT: 916671607, EVALUE 2.00e-91

OTHER INFORMATION: SWISSPROT HIT: P97303, EVALUE 1.00e-37

OTHER INFORMATION: EST_HUMAN HIT: BE890758.1, EVALUE 4.30e-01

US-09-864-761-32413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.4; DB 10; Length
Pred. No. 1.7e+02;
Mismatches 1; Indels
                                     PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: DCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-01-30
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                    APPLICATION NUMBER: PCT/US01/00661
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PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15909, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
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93.38;
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Best Local Similarity 93...
"hes 14; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 32413
LENGTH: 458
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Sequence 33413, Application US/09664761

PRICEAR TO SOOO 20048/63A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMBER: US/09/864,761

CURRENT PALICANTON NUMBER: US/09/864,761

CURRENT PILING DAYE: 2000-05-23

PRIOR PALICATION NUMBER: US 60/207,456

PRIOR APPLICANTON NUMBER: US 60/207,456

PRIOR PALICATION NUMBER: US 60/207,456

PRIOR PALICATION NUMBER: US 60/207,456

PRIOR PALICATION NUMBER: US 60/207,666

PRIOR PELING DAYE: 2000-09-26

PRIOR PALLICATION NUMBER: US 60/207,666

PRIOR FILING DAYE: 2000-09-27

PRIOR PILING DAYE: 2000-09-27

PRIOR PILING DAYE: 2001-10-30

PRIOR PILING DAYE: 2001-10-30

PRIOR PILING DAYE: 2001-01-30

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CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
COTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
CTHER INFORMATION: EXTRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXTRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXTRESSED IN PLACENTA, SIGNAL = 1.5
CTHER INFORMATION: EXTRESSED IN PLACENTA, SIGNAL = 1.5
CTHER INFORMATION: EXTRESSED IN PLACENTA, SIGNAL = 1.5
US-09-864-761-26040
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PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-39
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 26040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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OTHER INFORMATION: MAP TO AC006427.13
OTHER INFORMATION: EXPRESSED IN HEARY.
OTHER INFORMATION: EXPRESSED IN BLANG,
OTHER INFORMATION: EXPRESSED IN PLACER
OTHER INFORMATION: EXPRESSED IN PLACER
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93.3%;
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Best Local Similarity 93.3
Matches 14; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-09-864-761-32413
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Honsel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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COTHER INFORMATION: MAP TO ACO06427.13
COTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
COTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
COTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
US-09-864-761-9604
             PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ THAN SEQ ID NOS: 49117
SEQ THAN SEQ ID NOS: 49117
SEQ THAN SEQ ID NOS: 49117
SEQ ID NO 9604
LENGTH: 580
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93.3%; Pred. No. 1.8e+02;
live 0; Mismatches 1;
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PRIOR PELING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00670
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PRIOR APPLICATION NUMBER: PCT/US01/00661
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCTTCTCGCCCTGTT 15
                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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US-09-864-761-12426
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Honsheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-02-04
PRIOR PELING DATE: 2000-02-26
PRIOR PELING DATE: 2000-03-26
PRIOR PELING DATE: 2000-03-26
PRIOR PELING DATE: 2000-03-26
PRIOR PELING DATE: 2000-09-26
PRIOR PELING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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PRIOR FILING DATE: 2000-10-07
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                                                                     PRIOR FILING DATE: 2001-01-00
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 15909
LENGTH: 543
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Pred. No. 1.8e+02;
0; Mismatches 1;
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COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
US-09-864-761-15909
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                   PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
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PRIOR FILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00661
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93.3%;
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Matches 14; Conservative
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US-09-864-761-9604/c
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US-09-822-827-747/C

Sequence 747, Application US/09822827

Patent No. US20020081680A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C1

CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT PILLION DATE: 20011-03-28

NUMBER OF SEQ ID NOS: 982

SOGTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 747

LENGTH: 738
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APPLICANT: Hural, John
APPLICANT: MCHALL, Patricia D.
APPLICANT: MCHALL, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
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                  Indels
               1;
               Mismatches
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18-09-780-669-747/c
5. Sequence 747, Application US/09780669
Patent No. US20020051977A1
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OTHER INFORMATION: n=A,T,C or G
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Dillon, Davin C.
Mitcham, Jennifer L.
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Henderson, Robert A.
Kalos, Michael D.
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Vedvick, Thomas S.
Carter, Darrick
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Hepler, William
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Retter, Marc W.
Stolk, John A.
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Matches 14; Conservative
               Conservative
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                                                                        1 CCTTCTCGCCCTGTT 15
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ORGANISM: Homo sapiens
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               14;
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LENGIH: 738
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               Matches
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APPLICANT: Hoplus William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 747
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.98

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.92

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.85

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.85

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.75
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR RILICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 12426
LENGTH: 592
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Pred. No. 1.8e+02;
0; Mismatches 1;
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Patent No. US20020022248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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; LCCATION: (1)...(738)
; OTHER INFORMATION: n=A,T,C or G
US-09-759-143-747
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93.3%;
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Vedvick, Thomas S.
Carter, Darrick
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Retter, Marc W.
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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Best Local Similarity
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US-09-864-761-12426
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Sequence 1, Application US/09430029
Patent No. US20020168738A1
GENERAL INFORMATION:
TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,
TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,
TITLE OF INVENTION: Method for Degrading Chlorinated Aliphatic Hydrocarbon
TITLE OF INVENTION: Compounds and Aromatic Compounds, and
TITLE OF INVENTION: Compounds for Environmental Remediation
                            Gaps
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                            Indels
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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Pred. No. 1.9e+02;
      Pred. No. 1.8e+02;
); Mismatches 1;
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CURRENT FILING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: 06/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-27
PRIOR FILING DATE: 2000-112-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTERQ FOR WINDOWS VERSION 4.0
SEC ID NO 6020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: CF013982U$
CURRENT APPLICATION NUMBER: US/09/430,029
                                                                                                                                                                                                                Sequence 6020, Application US/09815242
Patent No. US20020061569A1
                          0;
                                                                                                                                                                                                                                                                                              Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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93.3%;
  93.38;
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                          14; Conservative
                                                                                    246 CCTCCTCGCCTGTT 260
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    Best Local Similarity
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Matches 14; Conserv
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US-09-430-029-1/C
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APPLICANT:
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600,438US1
CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
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APPLICANT: Xue, Y.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
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Pred. No. 1.8e+02;
0; Mismatches 1;
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Pred. No. 1.8e+02;
0; Mismatches 1;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 1458
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Patent No. US20020110897A1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
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                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(738)
CTHER INFORMATION: n=A,T,C or G
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93.3%;
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Best Local Similarity 93.3%;
Matches 14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
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TYPE: DNA
ORGANISM: Homo sapiens
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US-09-860-846-9
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APPLICANT: YAN, Chunhua et al.
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN AMINOTRANSFERASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: AND USES THEREOF
FILLE OF INVENTION: AND USES: 105/09/801,874
CURRENT PILICATION NUMBER: US/09/801,874
CURRENT FILLING DATE: 8001-03-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
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US-09-860-846-3/C
| Sequence 3, Application US/09860846
| Patent No. US20020164742A1
| SEQUENCE 3, APPLICANT
| APPLICANT: Liu, H.
| APPLICANT: Liu, Y.
| APPLICANT: Liu, Y.
| APPLICANT: Liu, Y.
| APPLICANT: Liu, Y.
| APPLICANT: Liu, H.
| APPLICANT: Liu, H.
| APPLICANT: Liu, N.
| APPLICANT: Liu, H.
| APPLICANT: Liu
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Pred. No. 2.1e+02;
0; Mismatches 1;
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                                                                                                                                                           ; Sequence 3, Application US/09801874
; Patent No. US20020048801A1
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93.3%;
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         4343 CCTTCTCTCCCTGTT 4357
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Best Local Similarity 93.3
Matches 14; Conservative
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Best Local Similarity
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                                                                                             RESULT 14
US-09-801-874-3/C
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LENGTH: 13613
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Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOO7
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
PILO APPLICATION CONS. 2442
SOFTWARE: Patentin Ver. 2.0
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93.3%; Pred. No. 2e+02;
Live 0; Mismatches 1;
                                     P1998-310801
CURRENT FILING DATE: 1999-10-29
EARLIER APPLICATION NUMBER: JP F
BARLIER FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PAtentin Ver. 2.1
                                                                                                                                                                                                                                               ORGANISM: Burkholderia cepacia
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NAME/KEY: CDS
LOCATION: (1803)..(3350)
OTHER INFORMATION: tomN
FEATURE:
NAME/KEY: CDS
LOCATION: (3428)..(3781)
OTHER INFORMATION: tomO
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Best Local Similarity 93.3
Matches 14; Conservative
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LOCATION: (463)..(1455)
COTHER INFORMATION: tomL
FEATURE:
NAME/KEY: CDS
LOCATION: (1495)..(1761)
OTHER INFORMATION: tomM
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NAME/KEY: CDS
LOCATION: (3810)..(4871)
OTHER INFORMATION: tomP
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OTHER INFORMATION: tomQ
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OTHER INFORMATION: tomK
FEATURE:
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ORGANISM: Homo sapiens
US-09-764-869-2353
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US-09-764-869-2353
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                                                                                                                                                        SEQ ID NO 1
LENGTH: 5828
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LENGTH: 5881
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1 CCTTCTCGCCCTGTT 15

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(without alignments)
146.257 Million cell updates/sec
                                                                                                                              December 11, 2002, 13:27:12 ; Search time 1661 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                     16154066 seqs, 8097743376 residues
                                                                                   OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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15
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em_estba:* EST: * Database

Maximum Match 100% Listing first 45 summaries

em_gss_mam: *
em_gss_mus: *
em_gss_other: * gb_est3:*
gb_est4:*
gb_est5:*
em_estfun:*
ep_est5:*
em_estom:*
gb_gss:*
em_gss_hum:* em_gss_inv:* em_gss_pln:* em_gss_vrt:* em_gss_fun:* em_esthum:*
em_estin:*
em_estmu:* em_estpl:*
em_estro:*
em_htc:* gb_est1:*
gb_est2:*
gb_htc:* em_estov:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_pro:* em_gss_rod:*

			Description	T48892 yb07a09.rl	BH019102 L2358k.d_	BM273267 if28e01.y	BH019101 L2357k.d_	AV434035 AV434035	BM142008 if25d08.y
SUMMARIES			ΩI		ВН019102	BM273267	ВН019101	AV434035	BM142008
			n :	14	17	13	17	10	13
			Match Length DB	309	313	505	513	543	551
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7 15 100.0 626 9 112 100.0 6258 113 100.0 6558 114 115 100.0 6558 114 115 100.0 6558 114 115 100.0 6558 114 115 100.0 6558 114 115 100.0 6558	BF971415 AA102111 AA099915 BI997613 BE313934	BE776197 BF315344 BC444893 BC609181 AG100084 BF180250 BG169177 AG085937	BG323915 BB068653 BB037017 BB054187 BB460985	BB464879 BB038101 AAJ0425 BB402819 BB105502 BB408502 AW436133 BF895478 CNS06WIC BB045638 BB403227	BQ693297 BB464805 AAA493073 BQ739202 W41213 BB472281 BB172281 BQ103252 BF743003 AI546215
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ALIGNMENTS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamania; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 309)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood, K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Genome Res. 6 (9), 807-828 (1996) 148892 TARRA Linear EST 06-FEB-1995 yb07a09.rl Stratagene placenta (#937225) Homo sapiens CDNA clone ILMAGE:70456 5' similar to SP:28778 S28778 COLLAGEN ALPHA 1(XV) CHAIN - HUMAN, mRNA sequence. Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu T48892 T48892.1 GI:650752 Contact: Wilson RK human. VERSION KEYWORDS SOURCE ORGANISM DEFINITION JOURNAL MEDLINE COMMENT REFERENCE AUTHORS RESULT 1 T48892/c ACCESSION TITLE

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Query Match
Best Local Similarity 100.
Matches 15; Conservative
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BM273267/c
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1 (bases I o 13)
Myler, P.J., Vogt. C., Cawthra, J., Klacking, M., Marty, A., Mack, J.,
Munden, H., Nguyen, D., Robertson, L., Sisk, E., Fazelinia, G., Aggarwal
G., Nelson, S., Seyler, A., Worthey, E. and Stuart, K.
Leishmania major Friedlin Cosmid End Sequences
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH019102
L2358k.d_HygT3.1 Leishmania major Friedlin Cosmid Genomic Library
Leishmania major genomic clone L2358k, DNA sequence.
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0
                                                                                                                                                                                                                                                                                                              /note="Organ: placenta; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dr. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
XR Vector: -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
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High qality sequence stops: 239
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RPl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="GDB491333"
/db_xref="LaXon:9606"
/clone="IMAGE:70456"
/clone="IMAGE:70456"
/clone="Ib="Stratagene placenta (#937225)"
/lab_host="SOLR cells (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                    5 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109-1651, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 15; DB 14;
100.0%; Pred. No. 6.1e+03;
tive 0; Mismatches 0;
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/organism="Leishmania major"
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                                                                                                      High quality sequence stop: 239.
Location/Qualiflers
1. 309
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/db_xref="taxon:5664"
/clone="L2358k"
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                                                                                                                                                                                                                                                                                                                                                                                               adaptor sequence: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 206 284-8846
Fax: 206 284-0313
Email: mylerpiebbri.org
Seq primer: Hyg73
Class: cosmid ends.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 503)

1 (Dases 1 to 503)

2 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hiller, L., Marra, M., Pape, D., Wylie, T., Marth, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gabbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

AL Ompublished (2000)

Other Ests: if28e01.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 12-MAR-2002
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA, 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BM273267 S05 bp mRNA linear EST 12-MAR-2C if 28e01.71 Melton Normalized Human Islet 4 N4 Hisl 1 Homo sapiens cDNA clone IMAGE:5677896 5' similar to SW:CALE.HUMAN P39059 COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR. [1] ;, mRNA sequence.
vector (Acc. No. CVU59231) is described in Ryan et al, Gene, 131:145-150 (1993)" 2 others
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                                                                                                                                                                      Score 15; DB 17;
Pred. No. 6.2e+03;
; Mismatches 0;
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Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
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                                                                                                                                                                             100.0%;
100.0%;
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and

Saga, N.

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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. .543
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Jackson, Y. and Bowers, R.,
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Porphyra yezoensis"
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/clone="Porphyra yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    AV434035 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone PM037d06_r 5', mRNA sequence.
                                                                                                                                                Bangiophyceae; Bangiales; Bangiaceae;
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                                                                                                                                                                                                                                        Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15; DB 10; Length 543;
Pred. No. 7e+03;
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Nikaido,I., Asamizu,E., Nakajima,M., Nakamura,Y.,
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                                                                                                                         Porphyra yezoensis
Eukaryota; Rhodophyta;
                                                              AV434035.1 GI:8589260
                                                                                                                                                                                                                                                                                                                              Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Other_ESTs: if25d08.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 c
                                                                                                        Porphyra yezoensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 15; Conservative
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Fax: 617-495-8557
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1 (bases I to 513)

Wyler, P. J., Vogt, C., Cawthra, J., Klacking, M., Marty, A., Mack, J., Munden, H., Nguyen, D., Robertson, L., Sisk, E., Fazelinia, G., Aggarwal, G., Nelson, S., Seyler, A., Worthey, E. and Stuart, K.
Leishmania major Friedlin Cosmid End Sequences
Unpublished (2000)

Contact: Myler PJ
. Junyle-stranded (unhybridized) plasmids were isolated hydroxyapatite chromatography and used to make this ynarv."
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L2357k.d_HygT3.1 Leishmania major Friedlin Cosmid Genomic Library
Leishmania major genomic clone L2357k, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: CLBYG; Site_1: BamHI; Genomic DNA from Leishmania major Friedlin was partially digested with Sau3AI. size selected, and ligated with BamHI-digested cLHYG cosmid vector DNA. 9216 clones were picked and arrayed. Library construction is described in Ivens et al., Genomics Research, 8:135-145 (1998). The CLHYG vector (Acc. No. CV95231) is described in Ryan et al, Gene, 131:145-150 (1993)"
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Friedlin"
/db_xref="taxon:5664"
/clone="1257k"
/clone="115"Leishmania major Friedlin Cosmid Genomic
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                     Length 505,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seattle Biomedical Research Institute
4 Nickerson Street, Seatttle, WA 98109-1651, USA
Tel: 206 284-8846
Fax: 206 284-0313
                                                                                                                       100.0%; Score 15; DB 13; 100.0%; Pred. No. 6.9e+03;
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/organism="Leishmania major"
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  20. Single-stranded by hydroxyapatite ch
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Seg primer: Hygr3
Class: cosmid ends.
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BH019101.1 GI:14197807
                                         library."
138 c
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                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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AV434035
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Gaps

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/note="Organ: Pancreas; Vector: pSPORTI; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using Superscript Plasmid Library kit (Life Technologies). CDNA made by oligo-dT prining. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on Solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; O.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by the single-stranded to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by the single-stranded (unhybridized).
Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brownefas.harvard.edu) This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov High quality sequence stops.

Seq primer: -40RP from Gibco High quality sequence stops: 144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
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602272934F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4361024 5',
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Dupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue procurement. ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov
Plate: LLAMI003 row: c column: 09

High quality sequence stop: 614.
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                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 617)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Islets of Langerhans"
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                                                                                                                                                                                                                                                   1. .551
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="Adult"
/lab_host="DH10B"
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BF971415.1 GI:12338630
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148 c
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/clone=TrMAGE:4561024"
/clone=lib="NIH_MGC_84"
/clone_lib="NIH_MGC_84"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="cross an adrenal gland; Vector: pCMV-SPORT6; Site_1:
Not1; Site_2: Sall; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 626)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Leg, M., Le, M., Le, N., Mardis, E., Moore, S., M., Martis, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA102111
zk87h09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:489857 3' similar to SW:CAlE_HUMAN P39059 COLLAGEN ALPHA 1(XV
) CHAIN PRECURSOR. ;, mRNA sequence.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Faxi: 314 286 1810
Faxi: 315 286 1810
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158 c 195 g 107 t
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/lab_host="DH10B"
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Lefebvre

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1031050H04.y2 C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                             Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                            Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebv. P., McDermott, J.P., Shrager, J., Sliflow, C. and Stern, D. Analyses of the Chlamydomons reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                                                                                                                                                                                                                                                     Chlamydomonadaceae; Chlamydomonas. 1 (bases 1 to 653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccular Plants. Project: 1031
Unpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
                                                                                                                                                                                                                                                                                            Chlamydomonas reinhardtii.
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                                            252 CCTTCTCGCCCTGTT 238
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                                                                                                                                                                                                                                                                                                             zk87h09.rl Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:489857 5' similar to SW:CA1E_HUMAN P39059 COLLAGEN ALPHA 1(XV AA099915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasoe, S., Dietrich, N., Duduque, T., Favello, A., Gish, W., Hawkins Stoe, S., Dietrich, N., Diadque, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, M., Hultman, M., Rucabo, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the INAGE Consortium (info@linge.llnl.gov) for further information.
Insert Length: 867 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
                                                                                                                                             Gaps
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went through one round of normalization. Library constructed by M. Fatima Bonaldo." 179 c 161 g 166 t 4 others
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                                                                                                    Length 626;
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/db_xref="GDB:3804444"
/db_xref=texon:9606"
/clone="IMAGE:489857"
/clone_lib="Soares_pregnant_uterus_NbHPU"
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100.0%; Pred. No. 7.2e+03;
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Location/Qualifiers
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/lab_host="DH10B"
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Best Local Similarity 100.
Matches 15; Conservative
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/clone_lib="cross_relation of the property of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                        /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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Email: chauser@duke.edu.
Location/Qualifiers
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us-09-750-609-9.rst

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/doc_lib="pinfestansMy"
/doc_stage="4 week old vegetative, non-sporulating
mycelium in synthetic medium"
/lab_host="E. coli, strain DH5-alpha"
/note="vector: pSPORT1; Site_1: Sal1; Site_2: Not1; Total
RNA was isolated from mycelium of P. infestans DBR7602
cultured for 4 weeks in synthetic medium. EST clones were
named by their position in the microtiter plate, preceded
by the prefix MY (for mycelial) and the successive number
of the microtiter plate (e.g. MY-06-A-04)."

180 c 198 g 151 t 3 others
                                         /organism="Phytophthora infestans"
/strain="DDR7602, A1 mating type"
/db_xref="taxon:4787"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:316255"
/clone=lib="NHH_MGC_19"
/tissue_type="neuroblastoma"
/lab_bost="nH108 (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI: cDNa made by oilgo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II: RT (Life Technologies).

Note: this is a NIH_MGC Library."
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MY-12-B-02 PinfestansMY Phytophthora infestans cDNA, mRNA sequence.
BE776197
                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Wageningen University
Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
Tel: 31 317 483 138
                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM122 row: c column: 04
High quality sequence stop: 618.
                                                                                                                              1 (bases 1 to 659)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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Kamoun,S., Hraber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F.
Initial assessment of gene diversity for the comycete pathogen
Phytophthora infestans based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
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/organism≂"Homo sapiens"
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Phytophthora infestans
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  BE313934.1 GI:9134434
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                                                                     Homo sapiens
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs rémail.nih.gov
Tissue Procurement. ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
High quality sequence stop: 644.

I. 713
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                           Gaps
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0
     Length 676;
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0
100.0%; Score 15; DB 12; 100.0%; Pred. No. 7.3e+03;
                                                                                                     0; Mismatches
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/db_xref="taxon:9606"
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BF315344
BF315344.1 GI:11263579
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100.0%;
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Query Match
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Matches 15; Conserv
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AUTHORS
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BQ609181.1 GI:21558520
                                                                                                                                                                BG444893 830 bp mRNA linear EST 15-MAR-2001 GA_Ea0025P19f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0025P19f, mRNA sequence.
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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 830)
Wing, R.A., Frisch, D. Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
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/clone=lib=ACossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
 Gaps
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100.0%; Pred. No. 7.7e+03;
Live 0; Mismatches 0;
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/organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 Jordan Hall, Člemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clemson University Genomics Institute
Clemson University
 Mismatches
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Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 182.
Location/Qualiflers
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BG444893.1 GI:13354545
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1 (bases 1 to 839)
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Conservative
                                  Best Local Similarity 100.
Matches 15; Conservative
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AUTHORS Clarke, B., Lambrecht, M. and Rhee, S.

JURNAL Assessing the utility of Arabidopsis genomic information for interpreting wheat EST sequences
JUGNAL Unpublished (2002)

COMMENT Tontect: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 348
Email: rheedacoma. Stanford.edu.
Location/Qualifiers
Source //Cultivar=Wyuum"
//Cultivar=Wyuum"
//Cultivar=Wyuum"
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//Cultivar=Wyuum"
//Cultivar=Wyuum"
//Clone_lib="wheat EST endosperm library"
//Lisaxon:456"
//Lisaxon:456"
//Lisaxon:456"
//Lisaxon:456"
//Lione_lib="wheat EST endosperm fissue 8, 10 and 12 DPA
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//Lisaxon:456"
//Lione_lib="wheat EST endosperm"
//Lione_lib="wheat EST endos
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version 5.1.3
- 2002 Compugen Ltd.
  GenCore
Copyright (c) 1993
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nucleic search, using sw model

OM nucleic

December 11, 2002, 13:30:57; Search time 2560.5 Seconds (without alignments) 147.290 Million cell updates/sec 49582208 24791104 seqs, 12571243825 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries IDENTITY_NUC Gapop 10.0 , Gapext 1.0 1 cettetegecetgtt 15 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 US-09-750-609-9 Title: Perfect score: Sequence: Scoring table: .. Searched: Database Run on:

cgn2_6/ptodatt2/pna/US6001_COMB.seq: cgn2_6/ptodatt2/pna/US6002_COMB.seq: cgn2_6/ptodatt2/pna/US6003_COMB.seq: cgn2_6/ptodatt2/pna/US6005_COMB.seq: cgn2_6/ptodatt2/pna/US6005_COMB.seq: cgn2_6/ptodatt2/pna/US6005_COMB.seq: cgn2_6/ptodatt2/pna/US6010_COMB.seq: cgn2_6/ptodatt2/pna/US6011_COMB.seq: cgn2_6/ptodatt2/pna/US6012_COMB.seq: cgn2_6/ptodatt2/pna/US6012_COMB.seq: cgn2_6/ptodatt2/pna/US6012_COMB.seq: cgn2_6/ptodatt2/pna/US6012_COMB.seq: cgn2_6/ptodatt2/pna/US6022_COMB.seq: cgn2_6/ptodatt2/pna/US6032_COMB.seq: cgn2_6/ptodatt2/pna/US6032_COMB.

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/cgn2_6/ptodata/2/pna/US6034_COMB.seq:*/cgn2_6/ptodata/2/pna/US6035_COMB.seq:*/cgn2_6/ptodata/2/pna/US6037_COMB.seq:*/cgn2_6/ptodata/2/pna/US6037_COMB.seq:*/cgn2_6/ptodata/2/pna/US6038_COMB.seq:*/cgn2_6/ptodata/2/pna/US6039_COMB.seq:*/cgn2_6/ptodata/2/pna/US6039_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 470, App	Sequence 470, App	Sequence 470, App	Sequence 309, App	Sequence 481, App	18784	Sequence 2923, Ap	Sequence 4005, Ap	Sequence 4006, Ap	Sequence 4007, Ap	Sequence 4008, Ap	Seguence 7016, Ap	Sequence 7017, Ap	Sequence 7016, Ap	Sequence 7017, Ap	Sequence 99, Appl	Sequence 104, App	Sequence 15, Appl
	ID		PCT-US00-35491-9	US-09-750-609-9	US-60-173-682-9	US-09-440-302A-470	US-09-440-302B-470	US-09-440-302-470	US-09-442-366A-309	US-09-698-012-481	US-09-534-856-18784	US-60-230-445-2923	US-09-948-933-4005	US-09-948-933-4006	US-09-948-933-4007	US-09-948-933-4008	US-09-634-306B-7016	US-09-634-306B-7017	US-10-027-632-7016	US-10-027-632-7017	US-60-175-854-99	US-60-175-854-104	PCT-US00-35491-15
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FEATURE:
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Sequence 9, Application PC/TUS0035491

GENERAL INPORMATION:
APPLICANT: ROBERTSON, DAVId
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: DAVID THERAPEUTIC METHODS RELATING THERETO
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC MOLETAL METHODS RELATING THERETO
TITLE OF INVENTION: DAVID MOLET: 2000-12-28
CURRENT APPLICATION NUMBER: PCT/OSO/35491
PRIOR APPLICATION NUMBER: 60/175,456
PRIOR PILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/173,682
NUMBER OF SEQ ID NOS: 40

SOFTWARE: PATENTIN VEY: 2.0
              Sequence 15, Appli
Sequence 15, Appli
Sequence 16550, A
Sequence 90, Appl
Sequence 90, Appl
Sequence 16300, A
Sequence 929, App
Sequence 929, App
Sequence 927, App
Sequence 127, Appl
Sequence 1027, Appli
Sequence 11, Appli
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APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC WITATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEDITIC METHODS RELATING THERETO
FILE REFERENCE: Attorney Docket No. 1242-27-2-2
CURRENT APPLICATION NUMBER: US/09/750,609
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: 60/175,456
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Sequence 1067, Ap
Sequence 1067, Ap
Sequence 18619, A
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100.0%; Pred. No. 1.3e+03;
Live 0; Mismatches 0; Indels
                 0 US-09-750-609-15

1 US-00-173-648-1

1 US-00-173-62-15

1 US-00-173-68-16

0 US-09-758-468-90

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US-09-440-302A-1067
US-09-440-302B-1067
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PCT-US00-35491-11
US-09-750-609-1
US-09-750-609-11
US-60-173-682-1
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    Best Local Similarity 100.
Matches 15; Conservative
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PCT-US00-35491-9
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SOFTWARE: Pat
SEQ ID NO 9
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Sequence 9, Application US/60173682

Sequence 9, Application US/60173682

GENERAL INFORMATION:

APPLICANT: Blakely, Randy D.

TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIGGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO FILE REFERENCE: Attorney Docket No. 1242-27

CURRENT FILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9
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100.0%; Pred. No. 1.6e+03;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.3e+03;
tive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Alex
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CIPII
CURRENT APPLICATION NUMBER: US/09/440,302A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 1193
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Nucleic Acid Probe
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/173,682
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
SEQ THARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 15
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ORGANISM: Artificial Sequence
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; ORGANISM: Homo sapiens
US-60-173-682-9
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Best Local Similarity
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Best Local Similarity
Matches 15; Conserv
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US-09-440-302A-470
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; ORGANISM: Homo sapiens
US-09-698-012-481
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                                                                                                                                                                                  APPLICANT: CHASHOW, MATVEY E.
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CIP11
CURRENT APPLICATION: Human NUMBER: US/09/440,302B
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 1193
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 470
LENGTH: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Marvey E.
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CIP11
CURRENT APPLICATION NUMBER: US,09/440,302
CURRENT FILING DATE: 1999-11-17
PRIOR FILING DATE: 1998-03-31
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 470
LENGTH: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Nucleic Acid Probe US-09-440-3028-470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Nucleic Acid Probe US-09-440-302-470
                                                                                                                               ; Sequence 470, Application US/09440302B
; GBNRRAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
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APPLICANT: Chenchik, Alex
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1 CCTTCTCGCCCTGTT 15
                  45 CCTTCTCGCCCTGTT 59
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US-09-440-302B-470
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APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Sellhamer, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Laura L.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
APPLICANT: POLYNUCLEOTIDES ENCODING OR REGULATING STRUCTURAL, SECRETED TITLE OF INVENTION: EXTRACELLULAR MOLECULES
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 481, Application US/09698012
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                             // Match 100.0%; Score 15; DB 18;
Local Similarity 100.0%; Pred. No. 1.6e+03;
hes 15; Conservative 0; Mismatches 0;
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Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION UNMBER: US/09/698,012;
CURRENT APPLICATION UNMBER: US/09/698,012;
CURRENT FILING DATE: 2000-10-27;
PRIOR APPLICATION NUMBER: 60/162,166;
NUMBER OF SEQ ID NOS: 9719-8;
SOFTWARE: FastSEQ for Windows Version 4.0;
LENGTH: 472;
APPLICANT: Lukashev, Matvey E.
TITLE OF INVENTION: Human Array
FILE REFERENCE: CLON-006CIP13
CURRENT APPLICATION NUMBER: US/09/442,366A
CURRENT FILING DATE: 1999-11-17
PRIOR FILING DATE: 1998-0331
NUMBER OF SEQ ID NOS: 2216
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 309
LENGTH: 258
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                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic gene fragment US-09-442-366A-309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: PD-1015 CIP
CURRENT APPLICATION NUMBER: US/09/534,856
CURRENT FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-534-856-18784/c
; Sequence 18784, Application US/09534856
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 CCTTCTCGCCCTGTT 59
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Gaps

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Sequence 4007, Application US/09948933
Sequence 4007, Application US/09948933
GENERAL INFORMATION:
TOTAL OF INVENTION: DILYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF ILLORDAND STEEL COOUTS
CURRENT ELLING DATE: 2000-99-10
PRIOR APPLICATION NUMBER: 60/231,399
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                      TESOL 1.12
Sequence 4006, Application US/09948933
Sequence 4006, Application US/09948933
Sequence 4006, Application US/09948933
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
TITLE OF INVENTION: DETECTION NO USES THEREOF
FILE REFERENCE: CL000787
CURRENT APPLICATION NUMBER: 60/231,399
PRIOR PLILING DATE: 2001-09-10
PRIOR PLILING DATE: 2000-09-08
NUMBER OF SEO ID NOS: 6404
SOFTWARE: FEALSEQ for Windows Version 4.0
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
Indels
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ilarity 100.0%; Pred. No. 1.7e+03;
Conservative 0; Mismatches 0;
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  Mismatches
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4007
LENGTH: 601
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; Sequence 4008, Application US/09948933
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 15; Conservative
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  Conservative
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                                            1 CCTTCTCGCCCTGTT 15
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Best Local Similarity
Matches 15; Conserv
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US-09-948-933-4007/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Human
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  15;
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    Matches
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Sequence 4005, Application US/09948933

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/948,933
CURRENT APPLICATION NUMBER: 00/231,399
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 6404

SOFTWARE: FEALSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATE: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPRENENCE: CLOOO765
CURRENT APPLICATION NUMBER: US/60/230,445
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 3051
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2923
LENGTH: 592
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Pred. No. 1.7e+03;
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                                                                                                                                                                                                                                                                                           100.0%; Score 15; DB 20;
100.0%; Pred. No. 1.6e+03;
Live 0; Mismatches 0;
                                                                                                                                          NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu01124269
                                                                                                                                                                                                                              ; OTHER INFORMATION: a, t, c, g, or other US-09-534-856-18784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2923, Application US/60230445 GENERAL INFORMATION:
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100.0%;
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Best Local Similarity 100.
Marches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 185 CCTTCTCGCCCTGTT 171
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SEQ ID NO 18784
LENGTH: 510
                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: 488
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US-60-230-445-2923
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; ORGANISM: Human
US-09-948-933-4005
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LENGTH: 601
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Gaps

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TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF TITLE OF INVENTION: DEFECTION AND USES THEREOF FILE REFERENCE: CLO00787.

CURRENT APPLICATION NUMBER: US/09/948,933

CURRENT FILING DATE: 2001-09-10

PRIOR FILING DATE: 2001-09-08

NUMBER OF SEQ ID NOS: 6404

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 601
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Sequence 7016, Application US/09634306B

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Delymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/09/634,306B

PRIOR FILING DATE: 2002-02-21

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-004-20

PRIOR PLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR SEQ ID NOS: 325720

SOFTWARE: FESLEEQ for Windows Version 4.0

SEQ ID NO 7016
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Query Match

100.0%; Score 15; DB 35; Length 601;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 15; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: December 11, 2002, 16:56:14 Job time: 2562.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 15; Conservative
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US-09-948-933-4008
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; ORGANISM: Human
US-09-634-306B-7016
                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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December 11, 2002, 13:38:27; Search time 88 Seconds (without alignments) 122:513 Million cell updates/sec
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                 IDENTITY_NUC Gapor 10.0 , Gapext 1.0
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                                                                                                                                                               Title:
Perfect score:
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                                                                OM nucleic
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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/cgn2_6/ptodata/1/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/USOS_NEW_COMB.seq:* Pending_Patents_NA_New:* Database :

chance to have a result being printed, Pred. No. is the number of results predicted by chance to becore greater than or equal to the score of the result beir and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 47407, A
Sequence 24273, A
Sequence 24273, A
Sequence 24268, A
Sequence 24268, A
Sequence 24267, A
Sequence 24272, A
Sequence 24272, A
Sequence 24272, A
Sequence 24271, A
Sequence 24277, A
Sequence 24277, A
Sequence 24267, A
Sequence 24267, A
Sequence 24266, A Appl Appl Appl Appl 75, Appl 1036, Ap Description Sequence Sequence Sequence Sequence S Sequence US-09-724-676-24268 US-09-724-676-24268 US-09-724-676-24272 US-09-724-676-24272 US-09-724-676-24271 US-09-724-6768-24271 US-09-724-6768-24271 US-09-724-6768-24267 US-09-724-6768-24267 US-09-724-676-24267 US-09-724-676-24267 US-10-284-499-14 US-09-513-999C-13316 US-10-271-889-52 US-09-724-676-24273 US-09-724-676A-24273 US-09-724-676-47407 PCT-US02-32727-4 US-10-057-498-4 US-10-201-365-22 DB Length 43338 43338 4848 4848 55222 55892 5642 6009 6152 61152 736 352 1458 1565 1565 2177 2520 5128 5132 7430 Query Match Score 113.4 113.4 113.4 113.4 113.4 113.4 113.4 Result ş 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 O 00

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C 27 134 69.3 1347 6 FFT-1087-3722-6 Sequence 29 134 69.3 1347 6 FFT-1087-3722-6 Sequence 29 134 69.3 13414 6 G 19-10-57-489-6 Sequence 21 134 69.3 13414 6 G 19-10-57-489-6 Sequence 21 134 69.3 13414 6 G 19-10-57-489-6 Sequence 21 13 66.7 1395 5 G 19-0-724-676-2316 Sequence 23 13 66.7 1395 5 G 19-0-724-676-2316 Sequence 23 13 66.7 25620 1 PCT-1052-324-05 Sequence 23 13 66.7 25620 1 PCT-1052-324-05 Sequence 23 13 66.7 25620 1 PCT-1052-32700-9 Sequence 24 12.4 62.7 26.1 26.0 26.0 20-24-676-2313-999-2344 Sequence 24 12.4 62.7 26.1 26.0 26.0 20-24-676-2313-999-2344 Sequence 24 12.4 62.7 26.1 26.0 26.0 20-10-24-676-1319-99-234-9 Sequence 24 12.4 62.7 26.1 26.0 26.0 20-10-24-676-1319-99-234-9 Sequence 24 12.4 62.7 26.1 26.0 26.0 20-10-24-676-1319-99-234-9 Sequence 24 12.4 62.7 26.1 26.0 26.0 20-123-999-234-9 Sequence 24 12.4 62.7 26.1 26.0 26.0 20-123-999-234-9 Sequence 24 12.4 62.7 26.7 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0	3, Appli 86, Appl 46, Appl 12, Appl 12, Appl 12, Appl 24360, A 24360, A 24360, A 24360, A 35734, A 35734, A 35734, A 35739, A 22349, A 22349, A 22349, A		Gaps 0;	Gaps 0;
27 13.4 89.3 9377 6 US-10-274-994-3 28 13.4 89.3 11347 1 FCU-USCO-2372786 30 13.4 89.3 11347 1 FCU-USCO-36692-12 31 34 89.3 11347 1 FCU-USCO-36692-12 32 13 86.7 1936 5 US-10-274-676-23136 34 13 86.7 1936 5 US-0-744-676-23136 35 13 86.7 1936 5 US-0-744-676-23136 36 13 86.7 276820 1 FCT-USCO-37700-2914 39 12.4 82.7 259 5 US-0-513-999C-2349 41 12.4 82.7 248 5 US-0-513-999C-2349 42 12.4 82.7 248 5 US-0-513-999C-2349 43 12.4 82.7 353 5 US-0-513-999C-2349 44 12.4 82.7 353 5 US-0-513-999C-2349 45 12.4 82.7 353 5 US-0-513-999C-2349 46 12.4 82.7 353 5 US-0-513-999C-2349 47 12.4 82.7 353 5 US-0-513-999C-2349 48 12.4 82.7 353 5 US-0-513-999C-2349 49 12.4 82.7 353 5 US-0-513-999C-2349 40 12.4 82.7 353 5 US-0-513-999C-2349 41 12.4 82.7 353 5 US-0-513-999C-2349 42 12.4 82.7 353 5 US-0-513-999C-2349 43 12.4 82.7 353 5 US-0-513-999C-2349 44 12.4 82.7 353 5 US-0-513-999C-2349 45 US-0-5-2-2-2-13-99C-2349 46 US-0-5-2-2-2-13-99C-2349 47 US-0-1-2-2-13-13-14-140 48 US-0-2-2-2-2-13-99C-2-2349 49 US-0-2-2-2-2-13-99C-2-2349 40 US-0-2-2-2-2-13-99C-2-2349 41 US-0-2-2-2-2-13-99C-2-2349 42 US-0-2-2-2-2-13-99C-2-2349 43 US-0-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-	sednence Sed		2876; 1s 0	2876; Ls 0;
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Squence 67, Application US/10133937

Squence 67, Application US/10133937

Squence 67, Application US/10133937

Specificant: Raingner, Markus

APPLICANT: Ringner, Markus

APPLICANT: Peterson, Carsten

APPLICANT: Peterson, Carsten

APPLICANT: Peterson, Carsten

APPLICANT: Meltzer, Paul

TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,

TITLE OF INVENTION: OTHER BIOLOGICAL STATES

FILE REFERENCE: 11613.560501

CURRENT APPLICATION NUMBER: US/10/133,937

CURRENT FILING DATE: 2002-11-04

NUMBER OF SEQ ID NOS: 99

SEQ ID NO 67

LENGTH: 5222
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                    Indels
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US-09-724-676A-24268/C
Sequence 24568, Application US/09724676A
Sequence 24568, Application US/09724676A
SEQUENCE INFORMATION:
TILLE OF INVENTION: Variants of alternative splicing
TILLE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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Pred. No. 53;
                      Mismatches
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Best Local Similarity 100.
Matches 15; Conservative
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US-10-133-937-67
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CORGANISM: Homo sapiens
US-09-724-676A-24268
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 15; Conserv
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US-10-133-937-67/c
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GENERAL INFORMATION:
FAPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENY APPLICATION NUMBER: US/09/724,676A
NUMBER OF SEQ ID NOS: 97222
SOFTWARE PatentIn version 3.2
SEQ ID NO 24273
LENGTH: 4338
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Sequence 24268 Application US/09724676

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen

CURRENT FAPLICATION NUMBER: US/09/724,676

UNMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin Version 3.2

SEQ ID NO 24268

LENGTH: 4848
                                                                                                    Sequence 24273, Application US/09724676;
GENERAL INFORMATION:
FRIEM TOMPURENT: COMPUGEN LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 24273
LENGTH: 4338
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      1422 CCTTCTCGCCCTGTT 1436
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US-09-724-676-24268
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CORGANISM: Homo sapiens
US-09-724-676A-24273
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US-09-724-676-24273
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US-09-724-676A-24273/c
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US-09-724-676-24268/c
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Score 15; DB 5; Length 5642;
Pred. No. 53;
Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181,4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILIG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24567
LENGTH: 6099
                      APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 1291814 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 24271
LENGTH: 5642
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TITLE OF INVENTION: Variants of alternative splicing
FILE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24267
LENGTH: 6099
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Pred. No. 53;
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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ORGANISM: Homo sapiens
US-09-724-676A-24267
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US-09-724-676A-24271
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US-09-724-676A-24267/c
        GENERAL INFORMATION:
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Sequence 24272, Application US/09724676A
GENERAL INFORMATION:
APPLICAN: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNMBER: US/09/724,676A
CURRENT FILNG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN VERSION 3.2
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Sequence 24271, Application US/09724676
GENERAL INFORMATION:
APPLICAN: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
SOFTWARE: PatentIN version 3.2
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US-09-724-676A-24271/c
: Sequence 24271, Application US/09724676A
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 9722
SOFTWARE: PatentIn version 3.2
SEO ID NO 24272
LENGTH: 5589
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US-09-724-676A-24272
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Best Local Similarity 100.0%; Score 15; DB 5; Length 6152;
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Sequence 24366, Application US/09724676A

GENERAL INFORMATION:
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENY APPLICATION NUMBER: US/09/724,676A

NUMBER OF SEQ ID NOS: 97222

SOFTWAREN FILING DATE: 2000-11-28

SOFTWARE: Patentin version 3.2

SEQ ID NO 24266

LENGTH: 6152
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Sequence 24266, Application US/09724676

Sequence 24266, Application US/09724676

Sequence 24266, Application US/09724676

TITLE OF INVENTION: Variants of alternative splicing

TITLE OF INVENTION: Variants of alternative splicing

TITLE OF INVENTION: Variants of alternative splicing

CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

SOFTWARE: PALEATIN VERSION 3.2

SOFTWARE: PALEATIN VERSION 3.2

SEQ ID NO 24266

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US-09-724-676A-24266
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CORGANISM: Homo sapiens
US-09-724-676-24266
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US-09-724-676A-24266/c
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GenCore version 5.1.3
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; Search time 2560 Seconds December 11, 2002, 17:01:38 - nucleic search, using sw model OM nucleic Run on:

(without alignments)
147.319 Million cell updates/sec

US-09-750-609-9 15 Perfect score:

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Total number of hits satisfying chosen parameters: 0 Word size :

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US-60-164-320-17650 US-60-183-791-17650 US-08-472-801-213 US-08-668-235-214 US-60-353-987-96987 US-60-353-987-969887 US-60-353-987-969887 US-60-353-987-969887 US-60-353-987-969887 US-60-353-997-969887 US-60-172-80-1062 US-60-172-80-2375-91887 US-60-172-3348-118	1 US-60-278-258-2470 1 US-60-324-185-15275 2 US-60-197-872-20101 2 US-08-803-6100-109 2 US-08-803-6100-109 2 US-08-803-6100-109 3 US-09-912-293-536 4 US-09-912-293-536 4 US-09-65-817A-29643 8 US-09-65-817A-29643 8 US-09-65-817A-26564 8 US-09-534-844-24680 PCT-USO1-00663-13580 PCT-USO1-00663-13580	2 US-09-565-306-73156 3 US-09-864-76-17150 3 US-09-864-76-17150 1 US-10-182-995-10392 1 US-10-182-995-10296 1 US-10-182-995-10296 2 US-10-203-135-12944 2 US-10-203-135-12944 2 US-10-203-135-136-1294 2 US-10-203-135-136-1294 2 US-10-203-139-13911 2 US-10-203-139-13911 2 US-00-203-139-13919 3 US-00-270-767-30602 6 US-09-270-767-30602 6 US-09-270-767-30692 6 US-09-270-849B-13850 0 US-09-270-767-30692 8 US-10-014-751-3349 8 US-10-014-751-3349	21 US-09-540-229-184998 90 US-60-253-654-31555 90 US-60-255-592-31555 18 US-09-478-821-4478 18 US-09-478-821-4478 18 US-09-74-300-7183 18 US-09-77-183 18 US-09-77-183 18 US-09-77-183 18 US-09-75-184-727 19 US-09-83-369-75-7 10 US-09-83-369-75-7 11 US-09-83-369-877 12 US-09-894-949-8777 13 US-09-894-949-8777 14 US-09-894-949-8777 15 US-09-894-949-8777 16 US-09-894-949-8777 17 US-09-894-949-8777 18 US-09-894-949-8777 19 US-09-894-949-8777 19 US-09-894-949-8777 10 US-09-894-949-8777 11 US-09-894-949-8777 12 US-09-894-949-8777 13 US-09-894-949-8777
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; OTHER INFORMATION: Nucleic Acid Probe US-09-440-302A-470
                                                                  Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO UNDERLYING PREPERTOR OF 1242-27-2-2 CURRENT APPLICATION NUMBER: US/09/750,609
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: 60/175,456
PRIOR APPLICATION NUMBER: 60/175,682
PRIOR APPLICATION NUMBER: 60/173,682
PRIOR FILING DATE: 1999-12-29
NUMBER: OF SEQ ID NOS: 40
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9
LENGTH: 15
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APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHODS RELATING THERETO
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
FILE REPERBENCE: Attorney Docket No. 1242-27
CURRENT APPLICATION NUMBER: US/60/173,682
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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63;
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Sequence 470, Application US/09440302A
Sequence 470, Application US/09440302A
APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Alex
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006C1P11
CURRENT APPLICATION NUMBER: US/09/440,302A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 1999-31
NUMBER OF SEQ ID NOS: 1193
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 470
LENGTH: 257
TYPE: DNA
TYPE: DNA
CREATURE: PRATURE: SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Pred. No.
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US-60-173-682-9
; Sequence 9, Application US/60173682
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;

Matches 15; Conservative 0
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Best Local Similarity 100.
Matches 15; Conservative
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GRGANISM: Homo sapiens
US-09-750-609-9
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ORGANISM: Homo sapiens
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Length 257;
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Pred. No. 57;
Wismatches 0; Indels
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DB 18;
57;
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100.0%; Pred. No. 57;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                            APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey E.
TITLE OF INVENTION: Human Neurobiology Array
TITLE OF INVENTION: Human Neurobiology Array
CURRENT ELLOR CLON-006CIP11
CURRENT APPLICATION NUMBER: US/09/440,302B
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 1193
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 470
LENGTH: 257
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GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Matvey E.
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CIPII.
CURRENT APPLICATION NUMBER: US/09/440,302
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 597
SEQ ID NO 470
LENGTH: 258
                                        Mismatches
Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Nucleic Acid Probe US-09-440-302B-470
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                                                                                                                                                                                                       US-09-440-302B-470; Sequence 470, Application US/09440302B; GENERAL INFORMATION:
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100.0%; Pr
tive 0;
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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Sequence 4005, Application US/09948933

Sequence 4005, Application US/09948933

GENERAL INFORMATION:
APPLICANT: VENTEN.
APPLICANT: VENTEN.
TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DATE: 2001-09-10
PRIOR APPLICATION NUMBER: (60/231,399
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 6404
SOFWARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 4005
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: USCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000765
CURRENT APPLICATION NUMBER: US/60/230,445
CURRENT APPLICATION NUMBER: US/60/230,445
SUPERENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 3051
SOFTWARE: FastSEQ for Windows Version 4.0
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         FILE REFERENCE: PD-1015 CIP
CURRENT APPLICATION NUMBER: US/09/534,856
CURRENT FILING DATE: 2000-03-24
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 26334
SEQ ID NO 18784
LENGTH: 510
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Best Local Similarity 100.0%; Score 15; DB 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu01124269
TITLE OF INVENTION: EXTRACELLULAR MOLECULES
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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-948-933-4005/c
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; ORGANISM: HUMAN
US-60-230-445-2923
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LENGTH: 592
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING STRUCTURAL, SECRETED, AND
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gearing, David P.;
APPLICANT: Gearing, David P.;
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2002-001;
CURRENT APPLICATION NUMBER: US/09/698,012
CURRENT APPLICATION NUMBER: 05/01202-001;
PRIOR APPLICATION NUMBER: 60/162,166
PRIOR FILING DATE: 12000-10-27
PRIOR PILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 9719
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                             APPLICANT: LUKASHOV, MALVEY E.
TITLE OF INVENTION: Human Array
FILE REFERENCE: CLON-006CIPJA
CURRENT APPLICATION NUMBER: US/09/442,366A
CURRENT FILING DATE: 1999-11.17
PRIOR PRIOR PRILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 2216
SOFTWARE: FastSED for Windows Version 4.0
SEQ ID NO 309
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                                                                 Sequence 309, Application US/09442366A GENERAL INFORMATION: APPLICANT: Chenchik, Alex
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Delegeane, Angelo M.
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Stuve, Laura L.
Mullahy, Sara J.
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-698-012-481
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Best Local Similarity
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                                            US-09-442-366A-309
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LENGTH: 472
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GENERAL INFORMATION:

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APPLICART: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CLO00787

CURRENT APPLICATION NUMBER: US/09/948,933

CURRENT FILING DATE: 2001-09-10

PRIOR APPLICATION NUMBER: 60/231,399

PRIOR FILING DATE: 2001-09-08

NUMBER OF SEQ ID NOS: 6404

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 4008
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GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: Delymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REPERBENCE: 108827, 129
CURRENT FILING DATE: 2002-02-21
FRICH REPETCATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-09-08-09
PRIOR FILING DATE: 1999-09-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR PELING DATE: 1999-08-09
PRIOR PELING DATE: 1999-08-08
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Pred. No. 56;
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100.0%; Pred. No. 55;
iive 0; Mismatches 0;
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Job time: 2589 secs
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-634-306B-7016/c
     US-09-948-933-4008/C
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; ORGANISM: Human
US-09-634-306B-7016
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GENERAL INFORMATION:
APPLICANT: VENTER.
TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
TITLE OF INVENTION: DEFECTION AND USES THEREOF
FILE REFERENCE: CLO00787
CURRENT APPLICATION NUMBER: US/09/948,933
CURRENT APPLICATION NUMBER: 60/231,399
PRIOR FILING DATE: 2001-09-08
NUMBER OF SEQ ID NOS: 6404
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CARDIOVASCULAR DISBASE AND LIPID DISORDERS, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO00787
CURRENT APPLICATION NUMBER: US/09/948, 933
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-09-08
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ive 0; Mismatches 0;
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LENGTH: 601
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4007
LENGTH: 601
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; ORGANISM: Human
US-09-948-933-4005
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; ORGANISM: Human
US-09-948-933-4007
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US-09-134-000C-1966
US-09-513-999C-35759
US-09-513-999C-32746
US-09-513-999C-32746
US-09-513-999C-32746
US-09-731-38A-338
US-09-724-676-15535
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US-09-724-676-45475
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US-09-724-676A-23436
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-09-724-676A-23443
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24272, A
24272, A
                                                                                                December 11, 2002, 17:10:08; Search time 88.5 Seconds (without alignments) 121.821 Million cell updates/sec
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24268,
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Matches 15; Conservative 0; Mismatches 0; Indels
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US-09-724-676-24273/C
; Sequence 24273, Application US/09724676
; General Information:
; TITLE OF INVENTION: Variants of alternative splicing
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REPERENCE: 120181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFFWARE: PatentIn version 3.2
; SEQ ID NO 24273
: LENGTH. 4338
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; Sequence 24273, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: ParentIn version 3.2
; SEQ ID NO 24273
; LENGTH: 4338
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GENERAL INFORMATION:
APPLICANY: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 24268
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SGRERAL INFORMATION:
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TITLE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin Version 3.2
SEQ ID NO 47407
LENGTH: 2876
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SEGREAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT ELLING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 47407
LENGTH: 2876
               US-09-724-676A-6617

US-09-724-676A-6619

US-09-724-676-6614

US-09-724-676A-6612

US-09-724-676A-6614

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Best Local Similarity 100.
Matches 15; Conservative
                1 CCTTCTCGCCCTGTT 15
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US-09-724-676A-47407
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US-09-724-676A-47407
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US-09-724-676-47407
    TYPE: DNA
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100.0%; Score 15; DB 5; Length 5589; 100.0%; Pred. No. 1.7;
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US-09-724-676A-24272/c
; Sequence 24272, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; TITLE OF INVENTION: Variants of alternative splicing
; TITLE OF INVENTION: Variants of alternative splicing
; CURRENT APPLICATION UNMER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SEQ ID NO 24272
; SEQ ID NO 24272
; LENGTH: 5589
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILIG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SEQ ID NO 24271
LENGTH: 5642
Sequence 24272, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 24272
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Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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Matches 15; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-09-724-676A-24272
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ORGANISM: Homo sapiens
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US-09-724-676-24271/c
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APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Peterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
FILE REPRENCE: 11613.560501
CURRENT-APPLICATION NUMBER: US/10/133,937
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin version 3.1
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                                                                                                         Score 15; DB 5; Length 4848; Pred. No. 1.7;
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US-09-724-676A-24268/C

Sequence 24268, Application US/09724676A

SEQUENCE 12468, Application US/09724676A

TTLE OF INVENTION:
TTLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: PATENTIN VETSION 3.2

SOFTWARE: PATENTIN VETSION 3.2
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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Best Local Similarity 100.
Matches 15; Conservative
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                                          ; ORGANISM: Homo sapiens US-09-724-676-24268
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US-09-724-676A-24268
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Best Local Similarity
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US-09-724-676-24272/C
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    LENGTH: 4848
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LENGTH: 5222
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                         TYPE: DNA
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                       Indels
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US-09-724-676-24266/C
Sequence 24266, Application US/09724676
Sequence 24266, Application US/09724676
SEMERAL INFORMATION:
APPLICANT: Compugen LTD
TILLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INFORMATION:
FILE REFERENCE: 129181.4 Compugen
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 24266
LENGTH: 6152
                     0;
    Pred. No. 1.7;
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                     0; Mismatches
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    100.08;
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Best Local Similarity 100.
Matches 15, Conservative
Best Local Similarity 100.
Matches 15; Conservative
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                                                             1 CCTTCTCGCCCTGTT 15
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; LENGTH: 6152
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24266
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Matches 15; Conserv
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US-09-724-676A-24266/c
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                                                                        US-09-724-676A-24271/C

Sequence 24771, Application US/09724676A

GENERAL INFORMATION

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SEQ ID NO 24271

LENGTH: 5642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24267, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24267
LENGTH: 6099
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Best Local Similarity 100.
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  2821 CCTTCTCGCCCTGTT 2807
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Best Local Similarity 100.
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-09-724-676A-24271
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US-09-724-676A-24267/C
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LENGTH: 6099
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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/cgn2_6/ptodata/2/pna/US6009_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US6029_COMB.seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 10, Appl	Sequence 10, Appl	10,	, Ap	Sequence 6, Appli	Sequence 5, Appli	Sequence 6, Appli	Sequence 5, Appli	9	Sequence 2932, Ap	Sequence 2932, Ap	Seguence 2907, Ap	Sequence 47840, A	Sequence 2907, Ap	Sequence 4668, Ap	Sequence 2311, Ap	Sequence 106084,	Sequence 150004,	Sequence 8529, Ap	Sequence 3885, Ap	Sequence 23661, A
OI.	PCT-US00-35491-10	US-09-750-609-10	US-60-173-682-10	PCT-US00-35491-5	PCT-US00-35491-6	US-09-750-609-5	08-09-750-609-6	US-60-173-682-5	US-60-173-682-6	US-09-306-349-2932	US-09-960-481-2932	US-09-076-667-2907	US-09-540-229-47840	US-60-048-002-2907	US-09-637-890-4668	US-09-652-918-2311	US-09-865-439A-106084	US-60-207-458-150004	US-09-552-086-8529	US-07-952-911-3885	US-09-293-972-23661
DB	П	29	61	٦	-	29	29	61	61	17	36	14	21	48	24	25	33	64	22	٣	16
% Query Match Length DB	15	15	15	41	41	41	41	41	41	197	197	248	248	248	327	327	355	355	376	393	393
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15
Result No.	-	7	e	4	c S	9	c 7	80	ი ი	10	11	12	13	14	c 15	c 16	c 17	c 18	c 19	20	c 21

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; ORGANISM: Homo sapiens
US-60-173-682-10
                                                                                                                                                             TYPE: DNA
CRCANISM: Homo sapiens
US-09-750-609-10
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US-60-173-682-10
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LENGTH: 15
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Sequence 10, Application PC/TUS0035491

GENERAL INFORMATION:
APPLICANT: Blakely Randy D.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATIC INTOLERANCE AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO FILE REFREENCE: Attorney Docket No. 1242-27 PCT
CURRENT APPLICATION NUMBER: PC1/0800/35491

CURRENT APPLICATION NUMBER: 60/175,456

PRIOR APPLICATION NUMBER: 60/175,456

PRIOR FILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn Ver. 2.0

LENTH: 15
Sequence 23661, A Sequence 11236, A Sequence 11236, A Sequence 11236, A Sequence 2488, Ap Sequence 2079, A Sequence 13056, A Sequence 9898, Ap Sequence 9898, Ap Sequence 10936, A Sequence 10936, A Sequence 15997, A Sequence 1599
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APPLICANT: Blakely, Randy D.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC WITATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPECTIC METHODS RELATING THERETO
FILE REFERENCE: Attorney Docket No. 1242-27-2-2
CURRENT APPLICATION NUMBER: US/09/750,609
PRIOR APPLICATION NUMBER: 60/175,456
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Sequence 998, App
Sequence 184, App
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US-09-565-240-8098
US-09-465-877-11236
US-09-906-555-11236
US-09-807-2488
US-09-657-2488
US-09-657-2488
US-09-465-877-13056
US-09-465-877-13056
US-09-906-555-13056
US-09-906-555-13056
US-09-906-555-13056
US-09-785-276A-9898
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US-09-546-817-10936
US-09-64-617-15997
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US-09-64-610-15997
US-09-634-3088-64600
US-10-027-638-64600
US-10-027-638-64600
US-10-027-638-64600
US-10-037-634-6100
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US-09-652-918-998
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            1 CCTTCTCCCCTGTT 15
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CORGANISM: Homo sapiens
PCT-US00-35491-10
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KEBULY 4

PGT-USOUS 5. Application PC/TUSO035491

SQUENCE 5. Application PC/TUSO035491

GENERAL INFORMATION:

APPLICANT: Robertson, David

APPLICANT: Robertson, David

TITLE OF INVENTION: GENETIC MUTATION UNDERLYING OFFHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO FILE REFERENCE: Attorney Docket No. 1242-27 PCT

CURRENT APPLICATION NUMBER: PCT/USO0/35491

CURRENT FILING DATE: 2000-01-12

PRIOR PELLING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: 60/175,456

PRIOR PILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PATENTIN VET. 2.0
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APPLICANT: Robertson, David
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
FILE REFERENCE: Attorney Docket No. 1242-27
CURRENT APPLICATION NUMBER: US/60/173,682
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
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100.0%; Pred. No. 2.6e+03;
Live 0; Mismatches 0;
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Pred. No. 3e+03;
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/173,682
PRIOR FILING DATE: 1999-12-29
WUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 10, Application US/60173682; GENERAL INFORMATION:
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Matches 15, Conservative
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; ORGANISM: Homo sapiens
PCT-US00-35491-5
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SERVEND INTOLNALIZOR.

DAPLICANT: RODERLESON, David

APPLICANT: Blakely, Randy D.

TITLE OF INVENTION: GENERIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO FILE REFERENCE: Attorney Docket No. 1242-27-2 CURRENT APPLICATION NUMBER: 05/09/750,609

CURRENT APPLICATION NUMBER: 05/09/750,609

PRIOR FILING DATE: 2000-12-28

PRIOR FILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PATENTIN VOT: 2.0

SEQ ID NO 6

LENGTH 41
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GENERAL INFORMATION:
APPLICANT: Robertson, David
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: BLAKELY, RANDY D.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
FILE REPERBNCE: Attorney Docket No. 1242-27
CURRENT APPLICATION NUMBER: US/60/173,682
NUMBER OF SEQ ID NOS: 15
SCHWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
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GENERAL INFORMATION:
APPLICANT: ROBERSON, David
APPLICANT: ROBERSON, David
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
FILE REPERENCE: Attorney Docket No. 1242-27
CURRENT APPLICATION NUMBER: US/60/173,682
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 41
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Pred. No. 3e+03;
Mismatches 0; Indels
  Sequence 6, Application US/09750609
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CORGANISM: Homo sapiens
US-60-173-682-5
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US-60-173-682-6/c
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US-60-173-682-5
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APPLICANT: Blakely, Randy D.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO FILE REFERENCE: Attorney Docket No. 1242-27-2-2 CURRENT APPLICATION NUMBER: US/09/750,609
CURRENT APPLICATION NUMBER: 06/175,456
PRIOR FILLING DATE: 2000-12-28
PRIOR FILLING DATE: 2000-01-11
PRIOR PLILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 41
                                                                                                                                                                                                                                   APPLICANT: Robertson, David
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC MUTATION UNDERLYING RELATING THERETO
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
FILE REFERENCE: Attorney Docket No. 1242-27 PCT
CURRENT APPLICATION NUMBER: PCT/US00/35491
CURRENT APPLICATION NUMBER: 60/175,456
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
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100.0%; Pred. No. 3e+03;
iive 0; Mismatches 0;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-750-609-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 15; Conserv
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US-09-750-609-6/c
15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 6
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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Matches
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APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Inggrid E.
APPLICANT: Maufachon, Rebecca E.
APPLICANT: Maufachon, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: HUMAN BRAIN
MUMBER OF SEQUENCES: 44483
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IPOPPY disk
COMPUTER: PROPERTION
COMPUTER: PROFILE PC-DOS/MS-DOS
SOFTWARE: WORD PERfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,667
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 15; DB 14; 100.0%; Pred. No. 3.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATORNEY AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0370P
TELECOMMUNICATION INFORMATION:
TELEFENDE: (415) 85-055
TELEFERX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 2907:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 47840, Application US/09540229
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Sturart, Susan G.
APPLICANT: Stuve, Laura I.
APPLICANT: Mullahy, Sara J.
                                                                                                                                                              Sequence 2907, Application US/09076667 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                       Gooding, Douglas H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 248 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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             1 CCTTCTCCCCTGTT 15
                                       3 CCTTCTCCCCCTGTT 17
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STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; IMMEDIATE SOURCE:
; CLONE: 3268389H1
US-09-076-667-2907
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US-09-540-229-47840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                         RESULT 12
US-09-076-667-2907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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| Sequence 2932 Application US/09960481
| Sequence 2932 Application US/09960481
| Sequence 2932 Application US/09960481
| Sequence 2932 Application US/09960481
| APPLICANT: Byrum, Joseph R. |
| APPLICANT: Byrum, Joseph R. |
| TITLE OF INVENTION: Plants J. |
| TITLE OF INVENTION: Plants |
| FILE REFERENCE: 38-21(15367)C |
| CURRENT APPLICATION NUMBER: US 09/306,481 |
| CURRENT FILING DATE: 2001-09-24 |
| PRIOR APPLICATION NUMBER: US 09/306,349 |
| NUMBER OF SEQ ID NOS: 53893 |
| SEQ ID NO 2932 |
| LENGTH: 197
                                                                                                                                                                                                                                                                                                          Sequence 2932, Application US/09306349
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Joseph R.
APPLICANT: Herk, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15367)B
CURRENT APPLICATION NUMBER: US/09/306,349
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 53893
SEQ ID NO 2932
LENGTH: 197
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Best Local Similarity 100.0%; Score 15; DB 36; Length 197;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 197
                                                                                    Length 41;
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                                                                                                                           0; Indels
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Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 0;
                                                                                  100.0%; Score 15; DB 61; 100.0%; Pred. No. 3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COTION: (1)..(197)
OTHER INFORMATION: unsure at all n locations;
THER INFORMATION: Clone ID: 701040886H1
US-09-960-481-2932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: unsure at all n locations (CTHER INFORMATION: Clone ID: 701040886H1 US-09-306-349-2932
                                                                                                                              Mismatches
                                                                                                                              ;
                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                         1 CCTTCTCCCCTGTT 15
                                                                                                                                                                                                                   28 CCTTCTCCCCTGTT 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-173-682-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                            US-09-306-349-2932
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Query Match
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Matches
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APPLICANT: Stuve, Laura L.

APPLICANT: Stuve, Laura L.

APPLICANT: Stuve, Laura L.

APPLICANT: Stuve, Laura L.

APPLICANT: Stuve, Laura V.

APPLICANT: Akerblom, Ingrid E.

APPLICANT: Akerblom, Ingrid E.

APPLICANT: Akerblom, Rebecca E.

APPLICANT: Riingler, Tod M.

TITLE OF INVENTION: HUMAN BRAIN

NUMBER OF SEQUENCES: 44483

CORRESPONDENCE ADDRESS:

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STREET: CALIFORNIA

COUNTRY: USA

ZIP.
APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS
FILE REPERENCE: PD-1033 CIP
CURRENT APPLICATION NUMBER: US/09/540,229
CURRENT FILING DATE: 2000-03-31
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEC ID NOS: 193582
SOFTWARE: PERL Program
SEC ID NO 47840
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 15; DB 21; Length 248; Best Local Similarity 100.0%; Pred. No. 3.7e+03; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC DOS/MS-DOS SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/048,002
                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00535318
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure

CATATON: 211

CATHER INFORMATION: a, t, c, g, or other

US-09-540-229-47840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0370P
TELECOMMUNICATION INFORMATION:
TELEFAN: (415) 845-0555
TELEFAN: (415) 845-4166
INFORMATION FOR SEQ ID NO: 2907:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 248 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCTTCTCCCCTGTT 15
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                 TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Shjan, Andrew W.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Galvin, Katherine
APPLICANT: Calvin, Katherine
APPLICANT: Calvin, Katherine
APPLICANT: Calvin, Katherine
APPLICANT: Leiby, Kevin R.
APPLICANT: Vasicek, Tom
APPLICANT: Vasicek, Tom
APPLICANT: Villeval, Jean-Luc M. G.
APPLICANT: Cepada, Mario
APPLICANT: Cepada, Mario
APPLICANT: Cepada, Mario
APPLICANT: Tepada, Mario
APPLICANT: Tepada, Mario
CURRENT: AND USES
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1152-001
CURRENT APPLICATION NUMBER: 05/147,939
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4668
LENGTH. 327
                                                                                                                       Ouery Match

100.0%; Score 15; DB 48; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels (
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100.0%; Pred. No. 3.8e+03;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: December 11, 2002, 16:56:15
Job time: 2561.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4668, Application US/09637890
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Shyjan, Andrew W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
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; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; CLONE: 3268389H1
US-60-048-002-2907
                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-09-637-890-4668/c
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us-09-750-609-10.rnpn

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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-264-237-1036
; Sequence 1036, Application US/10264237
; GENERAL IPCRMATION:
; APPLICANT: Birse et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13316, A Sequence 1036, Ap Sequence 1245, Ap Sequence 28339, A Sequence 24274, A Sequence 2247, Ap Sequence 2234, Ap Sequence 2234, Ap Sequence 2221, Ap Sequence 2246, Ap Sequence 2246, Ap Sequence 2246, Ap Sequence 2246, Ap Sequence 2245, Ap Sequence 2227, Ap Sequence 2227, Ap Sequence 2227, Ap Sequence 2237, Ap Sequence 2233, Ap
                                                                                                            (without alignments)
122.513 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                            2002, 13:38:27 ; Search time 88 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/USOS_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/USOS_NEW_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-724-676-24274
US-09-724-676-24274
US-09-724-676-2247
US-09-724-676-2234
US-09-724-676-2234
US-09-724-676-2234
US-09-724-676-2231
US-09-724-676-2221
US-09-724-676-2221
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US-09-724-676-38339
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-09-724-676-2245
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US-09-724-676-2220
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Maximum Match 100%
Listing first 45 summaries
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION WHOBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SOFTWARE: Patentin version 3.2 LENGTH: 1030
                                                                                                                                                                                                      APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 38339
LENGTH: 908
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Pred. No. 3.4e+02;
0; Mismatches 0;
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                                                                                                                                                                   Sequence 38339, Application US/09724676A GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-09-724-676A-38339
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Best Local Similarity
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US-09-724-676A-24274/C
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US-09-724-676-24274/c
                                                                                                                                    RESULT 5
US-09-724-676A-38339
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; ORGANISM: Homo s
US-09-724-676-24274
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LENGTH: 1030
TYPE: DNA
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100.0%; Score 15; DB 6; Length 25
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
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Sequence 1145, Application US/09620607B

GENERAL INFORMATION:
APPLICANT: Nehls, Michael
APPLICANT: Sambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Mutated Mammalian Cells and
TITLE OF INVENTION: Animals
FILE REFERENCE: LEX-0032-USA
CURRENT APPLICATION NUMBER: US/09/620,607B
CURRENT APPLICATION NUMBER: US 60/144942
PRIOR FILING DATE: 1999-07-20
PRIOR PLICATION NUMBER: US 60/144942
NUMBER OF SEQ ID NOS: 1848
SOFTWARE: PASTSEQ for Windows Version 4.0
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Sequence 38339, Application US/09724676
GENERAL INFORMATION:
APPLICARM: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 122181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILIG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SEQ ID NO 38339
LENGTH: 908
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Pred. No.
                                                                                                                                                                                            ; LOCATION: (99)...(99); OTHER INFORMATION: n equals a,t,9, or c us-10-264-237-1036
       PRIOR APPLICATION NUMBER: US 60/205,515 PRIOR FILING DATE: 2000-05-19 NUMBER OF SEQ ID NOS: 2876 SOFTWARE: PALENTIN VET. 3.1
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100.0%; Pre
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Best Local Similarity 100.
Matches 14; Conservative
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GRGANISM: Homo sapiens
US-09-724-676-38339
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CORGANISM: Mus musculus
US-09-620-607B-1245
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LENGTH: 2520
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; Sequence 2221, Application US/09724676A; GENERAL INFORMATION:
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Matches 14; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-724-676-2221
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SEQ ID NO 2234
LENGTH: 1667
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US-09-724-676A-2234/c
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     NUMBER OF SEQ ID
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LENGTH: 1667
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TITLE OF INVENTION: Variants of alternative splicing
TITLE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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GENERAL INFORMATION:
APPLICAT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
                                                   Score 14; DB 5; Le
Pred. No. 3.4e+02;
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                                       93.3%; Scc. 100.0%; Pred. No. ... 0; Mismatches
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; ORGANISM: Homo sapiens
US-09-724-676A-24274
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US-09-724-676A-2247
                                                                   Best Local Similarity
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US-09-724-676A-2247/c
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US-09-724-676-2247/c
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LENGTH: 1509
TYPE: DNA
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LENGTH: 1509
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2221
LENGTH: 1712
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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100.0%; Pred. No. 3.5e+02;
  DB 5; Le
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93.3%; Score 14; DB 5; Length 171
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2240
LENGTH: 1755
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE COMPUGEN LTD
TITLE REFERENCE: 129181.4 Compugen
CURRENY APPLICATION NUMBER: US/09/724,676
CURRENY FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE PATENT
SEQ ID NO 2240
LENGTH: 1755
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFWARE: Patentin version 3.2
SOFWARE: Patentin version 3.2
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CORGANISM: Homo sapiens
US-09-724-676-2240
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US-09-724-676-2240/c
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5504 5506 5506 5506 5506 5507 11 5511 5511 5512 5513 5516 5516 5516 5516 5516 5516 5516		n PC/T David andy David David ENETIC 2000-1 2000-01-6ER: 6	r. 2.0 s 100.0%; 100.0%; tive 15 15 15 an US/097 tin US/097
886.7 886.7 886.7 886.7 886.7 886.7 886.7 886.7 886.7 886.7 886.7 886.7		Application Application AATION: Robertson, BHTION: BHTION: ENTION: DISE: ATION NUMB	SOFTWARE: Patentin Ver. 2.0 TO ID NO. 10 TENGTH: 15 TYPE: DNA ORGANISM: Homo sapiens I CCTTCTCCCCTGTT 15 I CCTTCTCCCCTGTT 15 CCTTCTCCCCTGTT 15 CCTTCTCCCCTGTT 15 OO-750-60-10 SULT 2 OO-750-60-10 SEQUENCE 10, Application US/09750609 SENERAL INFORMATION: APPLICANT: ROBERTSON, DAVID APPLICANT: Blakely, Randy D.
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Gaps

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Length 41;

Score 15; DB 1; Pred. No. 2.9e+02; 0; Mismatches 0;

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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0
         ; TYPE: DNA; ORGANISM: Homo sapiens
PCT-US00-35491-5
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PCT-US00-35491-6/c
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GENERAL INFORMATION:
APPLICANT: Robertson, David
APPLICANT: Robertson, David
APPLICANT: BLAKely, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
FILL REPERBNOE: Attorney Docket No. 1242-27 PCT
CURRENT APPLICATION NUMBER: PCT/US00/35491
PRIOR APPLICATION NUMBER: 60/175,456
PRIOR APPLICATION NUMBER: 60/175,456
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO CURRENT APPLICATION NUMBER: US/09/750,609
CURRENT APPLICATION NUMBER: US/09/750,609
PRIOR FULING DATE: 2000-12-28
PRIOR FULING DATE: 2000-01-11
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
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APPLICANT: Robertson, David
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GRENTIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
TITLE OF INVENTION: DIAGNOSTIC NO. 1242-27
CURRENT APPLICATION NUMBER: US/60/173,682
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 10
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Pred. No. 2.8e+02;
; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-750-609-10
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US-60-173-682-10
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SEQ ID NO 5
LENGTH: 41
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LENGTH: 15
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RESULT 6

US-09-750-609-5

S Sequence 5, Application US/09750609

GENERAL INFORMATION:
APPLICANT: Blackly, Randy D.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
FILE REFERENCE: Attorney Docket No. 1242-27-2-2
CURRENT APPLICATION NUMBER: US/09/750,609

CURRENT FILING DATE: 2000-11-28

PRIOR PLICATION NUMBER: 60/175,456

PRIOR APPLICATION NUMBER: 60/175,456

PRIOR PLING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PATENTING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 40

SEQ ID NO 5

LENGTH: 41
                                                                                                                                                                                                    APPLICANT: Robertson, David
APPLICANT: Blakely, Randy D.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
TITLE OF INVENTION: DIAGNOSTIC AND 1240-27 PCT
CURRENT APPLICATION NUMBER: PCT/USO0/35491
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: 60/175,456
PRIOR FILING DATE: 1090-12-29
PRIOR FILING DATE: 1090-12-29
PRIOR FILING DATE: 1099-12-29
NUMBER: OF SEQ ID NOS: 40
SEQ ID NO 6
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100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 15; Conservative
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                      14 CCTTCTCCCCTGTT 28
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; ORGANISM: Homo sapiens
PCT-US00-35491-6
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US-09-750-609-5
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Indels

Length 41;

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APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Dlants
FILE REFERENCE: 38-21(15367)C
CURRENT APPLICATION NUMBER: US/09/960,481
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 09/306,349
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 53893
SEQ ID NO 2332
LENGTH: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Plants
FILE REPERBNCE: 38-21(15367)B
CURRENT APPLICATION NUMBER: US/09/306,349
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 53893
SEQ ID NO 2932
LENGTH: 197
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0; Mismatches 0;
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LOCATION: (1)..(197)
OTHER INFORMATION: unsure at all n locations
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CURRENT APPLICATION NUMBER: US/60/173,682 CURRENT FILING DATE: 1999-12-29 NUMBER OF SEQ ID NOS: 15 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 6
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Best Local Similarity 100.
Matches 15; Conservative
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ORGANISM: Glycine max
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Best Local Similarity
Matches 15; Conserv
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US-09-306-349-2932
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                                                                                                                          LENGTH: 41
                                                                                                                                                TYPE: DNA
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                                                                                                                                 Sequence 6, Application US/09750609

Sequence 6, Application US/09750609

GENERAL INFORMATION:
APPLICANT: BLAKELY, Randy D.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
TITLE REPRENCE: Attorney Docket No. 1242-27-2-2
CURRENT APPLICATION NUMBER: US/09/750,609
CURRENT FILING DATE: 2000-10-28
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VOICE: ADDITIONAL OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VOICE: ADDITIONAL OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VOICE: ADDITIONAL OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VOICE: ADDITIONAL OF SEQ ID NOS: 40
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APPLICANT: BLAKELY, RandY D.
APPLICANT: BLAKELY, RandY D.
TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
TITLE OF INVENTION: DIAGNOSTIC MUTATION UNDERLYING THERETO
FILE REFERENCE: Attorney Docket No. 1242-27
CURRENT APPLICATION NUMBER: US/60/173,682
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 15
SOGTWARE: PATCHIN Ver. 2.0
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 41
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US-60-173-682-6/C
US-60-173-682-6/C
; Sequence 6, Application US/60173682
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
; FILE REFERENCE: Attorney Docket No. 1242-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 15; DB 29; 100.0%; Pred. No. 2.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 5, Application US/60173682 ; GENERAL INFORMATION:
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Best Local Similarity 100.
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; ORGANISM: Homo sapiens
US-60-173-682-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens US-09-750-609-6
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                   CTTCTCCCCTGTT
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Best Local Similarity
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US-60-173-682-5
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APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS
FILE REFERENCE: PD-1033 SUNDER US/09/540,229
CURRENT APPLICATION NUMBER: US/09/540,229
CURRENT FILING DATE: 2000-03-31
Prior application data removed - refer to PALM or file wrapper
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: HUMAN BRAIN NUMBER OF SEQUENCES: 4483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 248;
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SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
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100.0%; Pred. No. 2.9e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00535318
NAME/KEY: unsure
LOCATION: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: a, t, c, g, or other US-09-540-229-47840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/60/048,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2907, Application US/60048002 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gooding, Douglas H.
Stuve, Laura L.
Stuart, Susan G.
Ito, Laura Y.
Akerblom, Ingrid E.
Delegeane, Angelo M.
Naughton, Rebecca E.
Klingler, Tod M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 855-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
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CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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LENGTH: 248
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STATE: CA
COUNTRY:
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APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
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                                                             Length 197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15; DB 14;
Pred. No. 2.9e+02;
                                                          Score 15; DB 36;
Pred. No. 2.9e+02;
                                                                                                     0; Mismatches
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; OTHER INFORMATION: Clone ID: 701040886H1
US-09-960-481-2932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTATION NUMBER: 39,132
REFERRNCE/DOCKET NUMBER: PD-0370P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 845-0555
TELEPHONE: (415) 845-4166
INFORMATION FOR SEQ ID NO: 2907:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-540-229-47840
; Sequence 47840, Application US/09540229
                                                                                                                                                                                                                                                                                    Sequence 2907, Application US/09076667 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: 3268389H1
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Best Local Similarity
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US-09-076-667-2907
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GEATION,
GENERAL INFORMATION;
APPLICANT: Slyjan, Andrew W.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Calvin, Katherine
APPLICANT: Clipepper, Janice A.
APPLICANT: Clipepper, Janice A.
APPLICANT: Wastcek, Tom
APPLICANT: Wastcek, Tom
APPLICANT: Willeval, Jan-Luc M. G.
APPLICANT: Milleval, Jan-Luc M. G.
APPLICANT: Mario
APPLICANT: Moyel Wario
APPLICANT: Mario
APPLICANT: Wario
AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Score 15; DB 48; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
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100.0%; Score 15; DB 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4668, Application US/09637890
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Shylan, Andrew W.
APPLICANT: Holtzman, Douglas A.
INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 248 bases pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
MMEDIATE SOURCE:
CLONE: 3268389H1
US-60-048-002-2907
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CORGANISM: Homo sapiens
US-09-637-890-4668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-637-890-4668/C
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           Sequence Seq
5-09-724-676A-2220

-09-724-676-2232

-09-724-676-2232

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1 73.3 1187 5 US-09-724-676A-1 1 73.3 1190 5 US-09-724-676-18 1 73.3 1190 5 US-09-724-676A-1 1 73.3 1193 5 US-09-724-676A-1 1 73.3 1193 5 US-09-724-676-18 1 73.3 1195 1 PCT-USO2-32432-4 1 73.3 1202 5 US-09-724-676-47 1 73.3 1202 5 US-09-724-676-47 1 73.3 1202 6 US-09-724-676-47	1 73.3 1210 6 US-10-255-403-69 1 73.3 1218 6 US-10-289-1448-3 1 73.3 1222 5 US-09-724-676-633 1 73.3 1222 5 US-09-724-676A-636 1 73.3 1222 5 US-09-724-676A-65 1 73.3 1224 6 US-109-724-676A-65 1 73.3 1224 6 US-109-724-676A-63 1 73.3 1251 5 US-09-724-676-145 1 73.3 1251 5 US-09-724-676-145	73.3 1261 5 US-09-724-676-238 73.3 1261 5 US-09-724-676-238 73.3 1266 5 US-09-724-676-228 73.3 1290 5 US-09-724-676-258 1 73.3 1290 5 US-09-724-676-258 1 73.3 1299 5 US-09-724-676-145 1 73.3 1299 5 US-09-724-676-145 1 73.3 1302 5 US-09-724-676-158 1 73.3 1302 5 US-09-724-676-258 1 73.3 1308 5 US-09-724-676-258 1 73.3 1308 5 US-09-724-676-258 1 73.3 1308 5 US-09-724-676-258	73.3 1308 5 US-09-724-676A-1851 73.3 1311 5 US-09-724-676-18515 173.3 1311 5 US-09-724-676-18515 73.3 1316 5 US-09-724-676-14534 73.3 1326 5 US-09-724-676A-1453 173.3 1326 5 US-09-724-676A-2581 73.3 1326 5 US-09-724-676A-2581 73.3 1327 5 US-09-724-676A-6495 73.3 1332 5 US-09-989-733-269 73.3 1332 5 US-09-999-643-269 73.3 1332 5 US-09-992-643-269 73.3 1332 6 US-09-992-643-269	1332 6 US-10-131-823A-4 1332 6 US-10-131-823A-4 1332 6 US-10-131-829A-4 1332 6 US-10-131-829A-4 1332 6 US-10-127-829A-4 1332 6 US-10-127-83A-4 1332 6 US-10-127-83A-4 1332 6 US-10-127-83A-4 1332 6 US-10-127-83A-4 1332 6 US-10-127-80A-4 1332 6 US-10-127-80A-4 1332 6 US-10-127-83A-4 1332 6 US-10-121-83A-4 1332 6 US-10-121-83A-4 1332 6 US-10-121-83B-4 1332 6 US-10-121-86-68A-4

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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PALENTIN VET: 3:1
SEQ ID NO 1036
LENGTH: 2520
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US-09-620-607B-1245/C

Sequence 1245, Application US/09620607B

Sequence 1245, Application US/09620607B

GENERAL INFORMATION:
APPLICANT: Nehls, Michael
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Zands, Arthur T.
TITLE OF INVENTION: Novel Mutated Mammalian Cells and
TITLE OF INVENTION: Animals
FILE OF INVENTION: Animals
CURRENT APPLICATION NUMBER: US/09/620,607B

CURRENT FILING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: US 60/144942

PRIOR APPLICATION NUMBER: US 60/144942

PRIOR PILING DATE: 1999-07-20

NUMBER OF SEQ ID NOS: 1848

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 248
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Sequence 38339, Application US/09724676

Sequence 38339, Application US/09724676

GENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676

UNUMBER OF SEQ ID NOS: 97222

SOFTWARE: PatentIn version 3.2

SEQ ID NO 38339

LENGTH: 908
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Pred. No. 28;
0; Mismatches (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (99)...(99)
USHER INFORMATION: n equals a,t,g, or
US-10-264-237-1036
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100.0%; Pre
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity
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                       Sequence 14538, A Sequence 14509, A Sequence 14522, A Sequence 14522, A Sequence 24662, A Sequence 24662, A Sequence 14514, A Sequence 14550, A Sequence 9011, Ap Sequence 9011, Ap Sequence 14528, A Sequence 25798, A Sequence 25798, A Sequence 25798, A Sequence 113, App Sequence 15798, A Sequence 15798, A Sequence 171, App Sequence 171, App Sequence 171, App Sequence 171, App Sequence 1658, A Sequence 1658, A Sequence 171, App Sequence 10561, A Sequence 10561
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APPLICANT: Dunalex Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
APPLICANTON: Expressed Sequence Tags and Encoded Human Proteins.
FILER REFERENCE: 59.052.RG
CURRENT APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 13316
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                            US-09-724-676A-14538

US-09-724-676-14509

US-09-724-676-14520

US-09-724-676-14522

US-09-724-676A-14522

US-09-724-676A-14514

US-09-724-676A-14514

US-09-724-676A-14514

US-09-724-676A-14514

US-09-724-676A-14514

US-09-724-676A-14528

US-09-724-676-1559

US-10-778-173-173

US-10-778-173-173

US-10-778-173-173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13316, Application US/09513999C GENERAL INFORMATION:
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; OTHER INFORMATION: r-a or g
US-09-513-999C-13316
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US-09-513-999C-13316/c
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Indels

Mismatches

DB 5; Length 1030; 27;

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Score 14;
Pred. No.
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 2000-11-28
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               NUMBER OF SEQ ID NOS: 97222
SOFWARE: Patentin version 3.2
SEQ ID NO 24274
LENGTH: 1030
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                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24274
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; ORGANISM: Homo sapiens
US-09-724-676A-2247
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Matches 14; Conserv
 CURRENT FILING DATE:
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Matches 14; Conserv
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SERENAL INFORMATION:
APPLICANT: Compugen LTD
TITLE REFERENCE: 129181.4 Compugen
FILE REFERENCE: 2000-11-28
CURRENT FILION NUMBER: US/09/724,676A
CURRENT FILION DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 38339
LENGTH: 908
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Sequence 24274, Application US/09724676

Sequence 24274, Application US/09724676

GENERAL INFORMATION:

TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION UNBER: US/09/724,676

CURRENT FILNG DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: PATENTING DATE: 1000-11-28
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
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100.0%; Pred. No. 27;
Live 0; Mismatches
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                                                               Score 14; DB 5;
Pred. No. 27;
                                                               Query Match 93.3%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 27; Matches 14; Conservative 0; Mismatches
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               ; ORGANISM: Homo sapiens US-09-724-676-38339
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US-09-724-676-24274
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Matches 14; Conserv
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US-09-724-676A-24274/C
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US-09-724-676A-38339
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US-09-724-676-2247/C

Sequence 2247, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 12181.4 Compugen

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 2247

LENGTH: 1509
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US-09-724-676A-2247/C

Sequence 2247, Application US/09724676A

SEQUENCE 2247, Application US/09724676A

SEQUENCE 2247, Application US/09724676A

TITLE OF INVENTION: Variants of alternative splicing

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2
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26;
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Mismatches
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US-09-724-676-2234/c
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Length 1755;
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                                  US-09-724-676A-2221/c
Sequence 2221, Application US/09724676A
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compagen
CURRENT FILLING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22211
SEQ ID NO 22211
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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Pred. No. 26;
0; Mismatches
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100.0%;
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Best Local Similarity 100.
Matches 14; Conservative
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CORGANISM: Homo sapiens
US-09-724-676A-2240
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CORGANISM: Homo sapiens
US-09-724-676-2240
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Best Local Similarity
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US-09-724-676A-2240/c
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICANT NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2221
LENGTH: 1712
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TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129414. Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN VERSION 3.2
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 2234
LENGTH: 1667
GENERAL INFORMATION:
APPLICANT: Compugen LTD
APPLICANT: Compugen LTD
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION WIDMBER: US/09/724,676
CURRENT APPLICATION WIDMBER: US/09/724,676
CURRENT ETLING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
END ID NO 2234
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Pred. No.
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US-09-724-676-2221/c
; Sequence 2221, Application US/09724676
; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-724-676-2221
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CORGANISM: Homo sapiens
US-09-724-676A-2234
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US-09-724-676-2234
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Matches 14, Conserv
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US-09-724-676A-2234/c
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